Release 2 Copyright D	.1D John F. Collins, Biocomputing Research Unit. (c) 1993, 1994, 1995 University of Edinburgh, U.K. vistribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a.	n.a. database search, using Smith-Waterman algorithm
Run on: Tu	Tue Dec 2 16:57:20 1997; MasPar time 425.56 Seconds
ular output not	generated.
Intle: >U. Description: (1 Perfect Score: 45 N.A. Sequence: Comp:	>US-08-915-004-12 (1-465) from US08915004.seq 465 1 ATGAACAAGTIGCTGTGCTGAGAIAGTIGTGACAGITTAG 465 TACTIGITCAACGACACGACTCTATCAACACTGTCAAATC
ole:	TABLE default Gap 6
Nmatch STD : Db	Dbase 0; Query 0
Searched: 36	362067 segs, 549138275 bases x 2
Post-processing: Mi	Minimum Match 0% Listing first 45 summaries
Database: em	embl-new3 1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC 17:VTR
Database: ge	18.BCT1 19.BCT2 20.BCT3 21.BCT4 22.BCT5 23.BCT6 24.BCT7 25.BCT8 27.BCT1 29.GEN1 30.GEN2 31.GEN3 32.HC7 33.HTG3 33.HT
	38:INV4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10 45:INV4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10 45:IVR7 42:INV11 46:IVR13 46:IVR7 43:IVR7 43
Database: ge	s:vrLt0 ank-new3 6:BCT 107:GEN1 2:MAM 113:VRT
Database: u	118:ROD 119:SYN 120:UNA 1 -emb150_99 122:part1
Statistics: M	Mean 10.226; Variance 3.862; scale 2.648
Pred. No. is t score greater and is derived	io. is the number of results predicted by chance to have a reater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query e Match	Length	DB	OI.			ed. No.
	7 7	90.0		57	128278 128278	rom	e n	85e-05 85e-05
	1010	. v.		26	RRMAP1B5	norvegicus mRNA	or	13e-02
Ω 4- τυ	7 (7	4 4	m	3.4	SFASSUBA CEC33B4	purpuratus mucraenorhabditis el	an	94e-01
	7	4.		61	CREPHOSRI	reinhardtii phos	of c	34e+00
~ 60	N (N	4 4		4 6 86	OCSF1/GN MMTNFR2A	O.cuniculus SF1/ ge M.musculus tumor ne	ecr 1.	34e+00
, O	7	4		118	MMTNFR2A	M.musculus tumor r	ecr 1	.34e+00
10	~ ~	4 4		6 C	MUSMINER2 MISINER1	Mouse tumor necrosi Murine tumor necros	is 1.	34e+00
12	1 (7)			86	MMMAP1B	Mouse MAP1B mRNA fo)r 1.	34e+00
	77	4.	-	83	HUMSEQX	Human microtubule-a	188 1.	34e+00
12	9 (3	. 4	4 M	37	CELK05B2	Caenorhabditis elec	yan 1.	34e+00
c 16	0.0	4.4	4	32	CEF36D3	*** SEQUENCING IN I	280 1.	34e+00 84e+00
c 18	4 (2)			19	DURTROPR	Datura stramonium	29k 5.	84e+00
	(4)	4.	,	63	MZEGSTIA2	Maize glutathione	5-t 5.	84e+00
210	1 (1	4 4	. 4	9 8	MLB1/30G HHU43400	Human herpesvirus-	7,	84e+00
1 (3	CI.	4	2	109	HS435D1	Human DNA sequence	* ;	3.84e+00
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0 25	4 (4	. 4		26	114734	Sequence 13 from pa	ate 2.	41e+01
(1)		4.		71	HS198H5R	H.sapiens CpG islan	2 L	41e+01
27	. • (-	4.4		v 6	HSLYCAL/ HTMGT212A	Human lysyl oxldds Homo sapiens GT212	an K	41e+01
1 (1	4 (4	. 4		41	DROANNX	D.melanogaster ann	exi 2	41e+01
30		4.		115	BPPT	B. pendula mRNA en	codi	2.41e+01
31 32	. • . •	4.4		777	SOYICL1A	Glycine max glyoxy	som 2	41e+01
33		4.		82	GPIDOPADDC	Guinea pig aromati	C-L	.41e+01
34		4.4		0 4 0 9	WHIRUBIAA BTU41320	T.aestivum fibulos Bos taurus mucin c	ore 2	.41e+01
,, .		4.		111	DMANX	D.melanogaster anxX g	, 6 XX	2.41e+01
ر م م	,,,	4.4		40	HUMAEPA	Homo sapiens anion	ex 2	.41e+01
000		4.			ACVNFDGK	Azotobacter chroco	2000	.41e+01
4 4	•••	4 4		. ~	•	Mouse mRNA for PC6	B, 2	.41e+01
42		4.				Azotobacter chroce	Ö	.41e+01
4 4 4 W 4 7		20 20 20 20 20 20 20 20 20 20 20 20 20 2	17013 36143 66990	37 40	EAAMASL CELT06C10 DRO14P	E.amylovara (Ea///4) Caenorhabditis elega Drosophila melanogas	E ti	2.41e+01 2.41e+01 2.41e+01
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					ALIGNMENTS			
RESULT LOCUS DEFINITI ACCESSIC	I NOITI	128278 Sequence 128278 91819054	2 5 from	15 b pat	p DNA ent US 55698	PAT 30.	30-0CT-1	-1996
KEYWORDS SOURCE ORGANI	SM	Unknown. Unknown.						
REFERENCE AUTHORS TITLE	F3 (0	Unclassif 1 (bases Bennett,A Plant inh	~ : - =	215) avito s of	ed. 1 to 215) , Labavitch,J.M., Powell. oitors of fungal polygal?	ell,A. and Stotz,H. galacturonases and	their	use to
JOURNA	. 7	control Patent:	fungal US 5569	dise. 830-	ase A 5 29-(:966		
FEATURE	RES		Locati		ualif			
BASE C	COUNT	15	/UIGall a	0 8	25 9	26 t 141 others		

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recombinant rat MAP 1B
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Best Local Similarity 76.1%;
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Jacobs, H.T.T.T.
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                                                                                         Submission
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                           gssktamtsrnrtgktannavdsrnmgdasvgsdkntkkhaknsadgkvgsknngdrnnr 180
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                                                                                                                                                          278 TCAAGCAGGAGTGCAAT-CGCACCACAACCGCGTGTGCGAATGCAAGGAAGGGCGCTAC 336
                                                                                                                                                                                                                   use to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 ATTCGCACACGCGGTTGTGGGTGCGATTGCACTCCTGCTTGACGTACTGCAGCTCCTTGC 260
                                                             mtnvtmssssvvsrtascndkakkdgnttsswttdccnrtwgvcdtdttyrvnndsghnk 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 †twgvcdtdttyrvnndsghnkyssanynyggnnvgaakthyythtnvsgadsktvtdsy 98
                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRMAPIB5 7095 bp RNA ROD 21-0CT-1992 R.norvegicus mRNA for microtubule associated protein IB. X60370 X60371 X60550
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Zauner, W., Kratz, J., Staunton, J., Feick, P. and Wiche, G.
Identification of two distinct microtubule binding domains on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases I to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
                                     5;
Match 6.0%; Score 28; DB 57; Length 215; Local Similarity 13.0%; Pred. No. 7.85e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 57; Length 215;
                                81; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 others
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55; Mismatches
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                                                                                                                                                                                                                                                                                  GCTGGTACGTGTCAATGTGCAGCAAAAT 424
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Best Local Similarity 17.0%;
Matches 23; Conservative
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Rattus norvegicus
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GMALNLEPDNVGVVVFGNDKLIKEGDVVKRSGAIVDVPVGESILGRVVDALGTPIDGK
                                                                                                                                               Submitted (07-AUG-1991) G. Wiche, Inst of Biochemistry, University of Vienna, Waehringerstrasse 17, 1090 Vienna, AUSTRIA
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S.purpuratus nuclear gene for mitochondrial ATP synthase subunit
alpha precursor.
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Strongylocentrotus purpuratus
Bukaryotae; Mitochondrial eukaryotes; Metazoa; Echinodermata;
Bukaryotae; Mitochondrial eukaryotes; Metazoa; Echinoida;
Strongylocentrotidae; Euechinoidea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
I (bases 1 to 2356)
Talamillo, A., Chisholm, A.A.R., Garesse, R. and Jacobs, H.T.
Expression of the nuclear gene encoding mitochondrial ATP synthas subunit alpha in early development of Drosophila and sea urchin
                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (07-AUG-1992) G. Wiche, Institute of Biochemistry and
Molecular Biology, University of Vienna, Dr. Bohrgasse 9, 1030
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/product="mitochondrial ATP synthase alpha subunit
/producor"
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/organise-"Strongylocentrotus purpuratus"
/organise-"embryo (early blastula, 14 hours)"
/clone_lib-"lambda ZAP, EH Davidson lab"
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mitochondrial ATP synthase alpha subunit; precursor.
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Eur. J. Cell Biol. 57 (1), 66-74 (1992) 92347374
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1856 c 1799 g 1:
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VIVSLLGGGAHVDFRNSEGGTAMHKAAFLSSFENVKTLIELGASPNYRDPIGLTPLYY
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EVVEFIQQAGDTITLKVITVDVADMSRGGTIVHRPPTDTHDAHGVDYYAPNEIRNAYS
ESRHASYRQRPGSGRRISAAELENLMVRQRVPSVQGSPYQMGYDQESLNGGYSSKKYN
SVSDMKRRKGORNVVASSAGLNRSTFEQAAPTTSTFEYNCSSRSTPQLSRMDSFDSFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASYSNINNINNSTTDFOMDLKNALAKRRSKVAHDVDEDEBRESRFĒGLSLRETVREN
VVERGKGIONIGIVNKKDSGYISSRTSLEPSESEEKDHRPHFSLDHSPNVQRVTLISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLEDNYGGKDNMSVASSSTASSSTVDLTKPGCFVVPSHVIPPVDYDDDPDSGTGDSD
GEIRCSEISFEHKKVDVWSVDDVIGWLSSLHLSEYTPAFRSGRINGRCLRQCDRSRFT
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KAGOKPOTVPDVSLPGQTASFTGRRAFNPFTHWCSAVYTBDLVDAWGAFGAVWGVNNH
GLWYRKNFDAFADAPLGSSDGMYQPFLSAASIGSEYDFSKIREVSGNFNLPIPGVNEL
FDFDGRFWYRGGGGTLINSAMERPLILSDPNBRAPYTFKYLNYMADRHMHYGHVVPNV
NLFVVGKDKIMERLMONRLNPTMVG"
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VGYVGLKELRDAMANIYVRGAVAPVKPDRKLISGTFLDMSHMNKDKLLNTPQTPPANG
LSINMESPRFGNSLTVPPMAL"
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/db_xref="PID:g6f1820"
/translation="MeINOKREEEDDDEMEWRRDGVKRDSNDFSNYCRQRSLSSDATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="PID:91066899"
/translation="DHVESNETFAEFCTRQAQNVVHFLVEDWFLSALLGIITAVLSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1016(19454..19683.20307..20460,20598..20745, 21230..22071,22309..22631,23139..23411.23469..23810, 23857..22445,24516..24617,24877..25146,25254..25313), 23857..25445,24516..24617,24877..25146,25254..25313), 2000 and a consideration of the construction of t
The start of this sequence (1..100) overlaps with the end of sequence CEBO491.

The end of this sequence (30012..30112) overlaps with the start of sequence CEC05D12.
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5947..6127,6408..6603))
/note="weak similarity with the E. coli outer membrane
protein FAED (Swiss Prot accession number P06970)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join (<1...4), 413...532,582..713,1122..1255,1465..1555,
1773..1844,1889..2204,2251..2494,2539..2629,2683..2867,
2916..3168,3214..3361,3418..3643,3693..3881,4265..4480)
/note="similar to chloride channel protein"
                                                                                                                                                                                                                                                                                                         /organism="Caenorhabditis elegans"
/clone="C33B4"
                                                                                                                                                                                                                                         location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="C33B4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome="II"
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2 (bases 1 to 30112)

2 (bases 1 to 30112)

3 Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Coulson, A., Craxton, M., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Laister, N., Laister, N., Laister, N., Laister, N., Laisten, M., Percon, J., Iloyd, C., McMurray, A., Mortimore, B., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, B., Staden, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Vaughan, R., Waterston, R., Watson, A., Weinstock, L., Walkinson-Sproat, J. and Wohldman, P., Wang, C., L., Milkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Control Sequence finishing criteria for the C. elegans genome current sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTIONS ARE THIS SEQUENCE IS NOT NECESSAILY THE ENTIRE INSERT OF CLONE C13B4. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. The true left end of clone C13B4 is at 1 in this sequence. The true right end of clone C13B4 is at 9858 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The true left end of clone C05D12 is at 30012 in this sequence. The true right end of clone B0491 is at 4602 in this sequence. Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green, ms in preparation), and other
                                                               VAIDTIINQKRFNDEAEEKNKLYCIVVÄIGOKRSTVAQIVKRLHDSDÄLKYTIIVSAT
ASDAAPLQYLAPYSGCAMGEFFRDNGKHALIIYDDLSKQAVAYRQMSLLLRRPPGREA
YPGDVFYLHSRLLERAAKMNPDFGGGSLTALPVIETOAGDSAXIPTNYISITDGQIF
LETELFYKGIPPAINVGLSVSRYGSAAQVKAMKQVAGSMKLDLGEYREVAAFAQFGSD
                                                                                                                                                                                                                                                               LDASTQNLLNRGVRLTELLKQGQYTPMAVEDQVAVLFAGVRGHLDKIDPAKVTKFEEQ
                     GPLGTEHRARVGTKAPGIPRISVREPMQTGIKAVDSLVLICRGQRELIIGDRQTGKTA
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Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
1 (bases 1 to 30112)
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/product-"mitochondrial ATP synthase alpha subunit
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                                                                                                                                                                                                                                                                                                                                    FLAHIRSSHQALLDTIRTEGQLSPQTEATLKDVVLKFLDTFEGʻ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2356;
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Pred. No. 2.94e-01;
Pred. .....rches 9; Indels
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Caenorhabditis elegans cosmid C33B4.
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Best Local Similarity 78.0%;
Matches 32; Conservative
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KEYWORDS

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O'Rand, M.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="phosphoribulokinase"
/db_xref="PiD:g167432"
/translation="NAFTMRAPAPRATAQSRVTANRARRSIVVRADKDKTVVIGLAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGCGKSTFMRRATSIFGGVPKPPAGGNPDSNTLISDWTTVICLDDYHCLDRNGRKVKG
YTALAFEANDYNDLANGWRALKEGKSVDKPIYNHVSGLIDAPEKIESPPILVIEGLHP
POKRDADNIOVLAPDDYGOLDFRAKTGNDMAERGHSLEISTRSSTAARKPDEDAYID
POKKDADNIIOVLAPDDKGOYLEVRLIHKEGSKMFDPVYLFDEGSTISMIPCGR
KALTCSFPGIKMEYGPDTWYGOEVSVLEMDGOPDKLEELIYUSSHLSNTSAKFYGEITO
OMLKNGGFPGSNNGTGLEOTIVGLKVPEVYERIVKKDVVPV"
                                                                                                    ö
                                                                                                                                                                                                                                                                     phosphoribulokinase.
C.reinhardtii, cDNA to mRNA.
Chlamydomonas reinhardtii
Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Chlorophyta;
Chlorophyceae: Volvocales; Chlamydomonas.
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                                                                                                    Gaps
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Euraryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eutaryotae; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 1255)
Richardson, R.T., Yamasaki, N. and O'Rand, M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-1995
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Location/Qualifiers
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                                                                Length 30112;
                                                                                                                                                                                                                         C.reinhardtii phosphoribulokinase mRNA, complete cds.
M36123
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                                                                        Pred. No. 2.94e-01;
0; Mismatches 9; Indels
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Pred. No. 1.34e+00;
0; Mismatches 17; Indels
                                                                                                               Db 14748 ctgtaaaaactattgtactttgcatgttactcattactttt 14788
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Chlamydomonas reinhardtii"
                                                                                                                                 MAM
                                                              Score 23; DB 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="phosphoribulokinase"
28.1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product="phosphoribulokinase"
                   9126 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 t
QLGVTRIAHRQIIESALRGLLQ
                 5799 g
                                                                                                                                                                                                                 mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA
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O.cuniculus SP17 gene.
Z20655
                                                                                                                                                                                                              1245 bp
                                                          / Match
Local Similarity 78.0%;
hes 32; Conservative
              5271 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 69.6%;
Matches | 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 c
                                                                                                                                                                                                                                                                                                                                                                                                                                          1..1245
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           9916 a
                                                                                                                                                                                                            CREPHOSRI
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                                                      Query Match
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                                                                                     Matches
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Submitted (21-7aN-1993) O'Rand M. G., University of North Carolina at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel Hill, North Carolina, USA, 27599-7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (29-APR-1994) O'Rand M. G., University of North Carolina
at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel
Hill, North Carolina, USA, 27599-7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="pid::4479084"
/db_xref="pid::4479084"
/db_xref="swiss-prot::p36425"
/db_xref="swiss-pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="3' untranslated region is identical for both 0.9 KB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="alternate 5' untranslated region for 0.9 KB mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="alternate 5'untranslated region for 1.1 KB mRNA" 607...1047
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION M.musculus tumor necrosis factor receptor 2 mRNA. ACCESSION X76401
localization during the acrosome reaction Dev. Biol. 165 (2), 688-701 (1994) 95046885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryctolagus cuniculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22; DB 47;
Pred. No. 1.34e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="New Zealand white"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="testis"
/cell_type="spermatogenic"
/clone_lib="Rabset"
/clone="SR-1&R-16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND 1.1 KB mRNAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="SP17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (bases 1 to 1256)
O'Rand, M.G.
                                                                                                                                                                              (bases 1 to 1256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1388 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                   revised by [3] MAT
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es 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /qermline
                                                                                                                                                                                                                                                             Direct Submission
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168 ctcggacaccgtgtgtgc 185

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/translation="LWATGHTVPAQVVLTPYKPEPGYECQISGEYYDRKAQMCCAKCP
PGQYVKHFCKKTSDTYCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRACTKQQNR
VCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCRACAPGTFSDTT
SSTDVCRPHRICSILAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQPLDQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSCLORDARVPHVPDEKSODAVGLEOQHLLTTAPSSSSSSLESSASAGDRRAPPGGHP
QARVMAEAQGSQEARASSRISDSSHGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATV
GDPDAKPSASPKDEQVPFSQEECPSQSPYETTETLQSHEKPLPLGVPDMGMKPSQAGW
                                                                                                                   Powell.E.E., Wicker,L.S., Peterson,L.B. and Todd,J.A. Allelic variation of the type 2 tumor necrosis factor receptor gene Mamm. Genome 5 (11), 726-727 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPSQTPSILTSLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCFILVQRKKK
           Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A.
Amino acid variation in the tumor Necrosis factor receptor 2 is
linked to autoimmune diabetes in NOD mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace(1143, "t")
/gene="murine tumour necrosis factor receptor 2"
/note="silent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(1262, "g")
/gene="murine tumour necrosis factor receptor 2"
/note="Thr to Cys"
replace(1317, "g")
/gene="murine tumour necrosis factor receptor 2"
/note="silent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace(1047, "t")
/gene="murine tumour necrosis factor receptor 2"
/note="silent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="murine tumour necrosis factor receptor 2" /note="silent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="murine tumour necrosis factor receptor 2" /note="Thr to 11e"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="murine tumour necrosis factor receptor 2"
/note="Ser to Thr"
replace(278, "t")
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                                                                                                                                                                                                                                                                                                                                     /gene="murine tumour necrosis factor receptor 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="murine tumour necrosis factor receptor /note="Phe to Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene≂"murine tumour necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="murine tumour necrosis factor receptor
                                                                                                                                                                                                                                                                                                /chromosome="4 (distal region)"
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                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/db_xref="PID:9433831"
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                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="silent"
replace(975,"c")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replace(260, "c")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(802, "a")
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                                                                                                                                                                                                                                                                              /strain="NOD
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(bases 1 to 1388)
                                                                                                     (bases 1 to 1388)
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                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                         JOURNAL
MEDLINE
  REFERENCE
                      AUTHORS
                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                    FEATURES
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                                             TITLE
                                                                                                                                                    TITLE
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3 (bases 1 to 1388)
Powell, E.E., Wickerf.L.S., Peterson, L.B. and Todd, J.A.
Allelic variation of the type 2 tumor necrosis factor receptor gene
Mamm. Genome 5 (11), 726-727 (1994)

Powell, E.E.
Direct Submission
Submitted (26.NOV-1993) E.E. Powell, c/o John Todd, Level 6
Nuffield Dept of Surgery, The John Radcliffe Hospital, Oxford, UK
Nuffield Dept 1388)
2 (bases 1 to 1388)
Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A.

Amino acid variation in the tumor Necrosis factor receptor 2 linked to autoimmune diabetes in NOD mice

Unpublished

JOURNAL REFERENCE

AUTHORS TITLE

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;

(bases 1 to 1388)

Mus.

AUTHORS

JOURNAL REFERENCE

TITLE

REFERENCE

17-FEB-1997

MMINERZA 1388 bp RNA ROD M.musculus tumor necrosis factor receptor 2 mRNA. X76401

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RESULT

DEFINITION

ACCESSION

KEYWORDS

SOURCE

tumour necrosis factor receptor

9433830

Mus musculus house mouse.

ORGANISM

//Tablaidide.

/gene="murine tumour necrosis factor receptor 2"

/db_xref="PID:9433831"

/codon_start=1

/chromosome="4 (distal region)"

/organism="Mus musculus"

/strain="NOD"

<1..1380

Location/Qualifiers

95178848

MEDLINE

TITLE JOURNAL

AUTHORS

..1388

source

/gene="murine tumour necrosis factor receptor 2" /note="Ser to Thr" .replace="c" 278

FDQIAVKVA"

variation

variation

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/gene="murine tumour necrosis factor receptor /note="Thr to Ile"

'replace-"t"

variation

/gene="murine tumour necrosis factor receptor

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/gene="murine tumour necrosis factor receptor 2"
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                                           /gene="murine tumour necrosis factor receptor/note="Phe to Ile"
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/note="silent"
/replace="t"
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/replace="a"
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EYIDRKAQMCCAKCPPGQYVKHFCNKTSDTVCADCEASMTTQVWNQFRTCLSCSSSCT
TDQVEIRACTKQONRYCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGN
VLCKACAPGTFSDTTSSTDVCRPHRICSILAIPGNASTDAVCAPESPTLSAIPRTLYV
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Lewis,M., Tartaglia,L.A., Lee,A.L., Bennett,G.L., Rice,G.C., Wong,G.H.W., Chen,E.Y. and Goeddel,D.V.
Cloning and expression of cDNAs for two distinct murine necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 FCAGCTGTTGTGTGACAAATGTCCTCCTGGTACCTACCTAAACAACAACACTGTACAGCAAA 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor receptors demonstrate one receptor is species specific
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834 (1991)
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Mouse tumor necrosis factor receptor 2 mRNA, complete cds.
M60469
                                                  /gene="murine tumour necrosis factor receptor 2"
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/note="silent"
/replace="t"
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Pred. No. 1.34e+00;
0; Mismatches 28; Indels 0;
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Mus musculus
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/replace="g"
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/note="silent"
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Best Local Similarity 64.1%;
Matches 50; Conservative
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GADWOLITVQPKKKRESCAGABAKVPHVPDBKSQDAVGLEQQHLLTTAPSSSSSLES
SASAGDRRAPPGGHPQARVMAEAQGFQEARASSRISDSSHGSHGTHVWYTCIVWVCSS
SDHSSQCSSQASATVGDPDARRSASKDEQVPFSQEECPSQSPCETTETLQSHEKPLP
LGVPDMGMKFSQAGWFDQIAVKVA"
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases I to 3796)
Goodwin,R.G., Anderson,D.M., Jerzy,R., Davis,T., Brannan,C.I.,
Copeland,N.G., Jenkins,N.A. and Smith,C.A.
Molecular cloning and expression of the type 1 and type 2 murine
receptors for tumor necrosis factor
Mol. Cell. Biol. 11, 3020-3026 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                    MUSTNFR1 3796 bp mRNA ROD 01-AUG-1991
Murine tumor necrosis factor I receptor (TNFR-1) mRNA, complete
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Pred. No. 1.34e+00;
0; Mismatches 28; Indels
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Pred. No. 1.34e+00;
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Mus musculus lymphoid cDNA to mRNA.
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/cell_type="helper T-cell"
/tissue_type="lymphoid"
/map="Chromosome 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGVPDMGMKPSQAGWFDQIAVKVA"
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Best Local Similarity 64.1%;
Matches 50; Conservative
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g ô ద ò RESULT

SOURCE

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Homo sapiens
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LIEDEEKLKETQPGERVVIQKETEVSKGSAESPDEGITTTEGEGECEQTPEELEPVEK
QGVDDIEKFEDEGAGFEESSETGDYEEKAETEEAEEPEEDGEDNASGSASKHSPTEDD
ESAKAEADVHLKEKRESVVSGDDRAEEDMDDVLEKGEAEQSEEGGEEEDKAEDAREEG
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GGSESEATASDEENREDQPEEFTATSGYTQSTIGISSEPTPMDEMSTPRDVMSDETNN
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VPDSESPVEKVLSPLRSPPLLGSESPYEDFLSADSKVLGRRSESPFEGKNGKQGFPDR
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EKTPLGERSVNFSLTPNEIKVSAEGEARSVSPGVTQAVVEEHCASPEEKTLEVVSPSO
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Submitted (09-3AN-1990) Cowan N.J., Dept. of Biochemistry, New York
University Medical Center, 550 First Avenue, New York, NY 10016
(bases 1 to 7620)
Doble, M., Lewis, S.A. and Cowan, N.J.
The microtubule binding domain of microtubule-associated protein
Maple contains a repeated sequence motif unrelated to that of MAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Verțebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
ö
                                                                                                      195 tcagatgtgctgqtgctaagtgtcctcctggccaatatgtgaaacatttctgcaacaagac 254
                                                                                                                                                                                                                                                                                                                                                                                   MMMAP1B 8818 bp RNA ROD 12-SEP-1993
Mouse MaP1B mRNA for MAP1B microtubule-associated protein.
X51396
       Gaps
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       0; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAP1B gene; microtubule-associated protein.
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54..7448
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/strain="Swiss Webster"
/dev_stage="5 day old"
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/clone_lib="lambda GEM"
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/db_xref="PID:q53000"
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                                                                                                                                                                                                                     255 ctcggacaccgtgtgtgc 272
              50; Conservative
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JOURNAL
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ILPEMEGLSETEYLSESVEYPSPFDILEPPTSGGFIKLSKPCCYIFPGGRGDSALFA
VNGFNALINGGSERKSCFWKLITRHLDRVDSILLTHIGDDNLPGINSMLQRK ABLEEE
OSGGSTTNSDMMKNLISPDLGVVFLWYPENLKNFRSTEBAGFTLQYLNKLS
PILPNGGEVDLPISYLLSVESCHIVWHPNLKNFRSTEBAGFTLQYLNKLS
FILPNGGEVDLPISYLTSVSSLIVWHPANPARKIIRVLFPGNSTQYNILEGLEKLKHL
DPLRQPLATQKDLIGQVPTPVVKQTKLKQRADSRESLKPAARPLPSKSVRKSKESTP
EVTKVNHVEKPPRVESKEKVMVKKDKFPVKTETKPSVTEKEVSKESTFRETT
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VGTGATTAAVMAAAGIAAIGPAKELEAERSLMSSPEDLTKDFEELKAEEVDVTKDIKP
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VEKOGVDDIEKFEDEGAGFEESSETGDYEEKAETEEAEFEDGEEHVCVSASKHSPT
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biyteehlrraignielgirswdtnliecnldoelklfvsrhsarfspevpgokilhh
rsdyletyvlinpsdeavstevrlmitdaarhkllvlgocfentgelilosgsfsfo
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Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
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TRGEEKDKETKNAANASASKSAKTATTGPGTTKTAKSSTVPPGLPVYLDLCYIPNHSN
SKNVDVEFFKRVRSSYYVVSGNDPAAEEPSRAVLDALLEGKAQWGSNMQVTLIPTHDS
ESPVSDLTSTGLYODKOEEKSTGFIPIKEDFGPEKKTSDVETMSSQSALALDERKLGG
DVSPTQIDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGVAEDTYSHMEGVASVSTAS
VATSSFPEPTTDDVSPSLHAEVGSPHSTEVDDSLSVSVVQTPTTFQETEMSPSKEECP
                                                                                                                                                                             RPMSISPPDESPKTAKSRIPYODHRSEQSSMSIEFGGESPEHSFAMDFSRGSPDHPTL
GASVLHITENGPTEYDXSPCDIQDSSLSHKIPPTEBESYTODNDLSELISVSQYBASP
STSAHTPGOGARSPLQEDTLEDVVPPREMSLYASLASEKVQSLEGEKLSPSTSPLT
PRESSPLISPGFENSTRAAKETAAAHQASSSPPIDAATAEPYGFRSMLEDTMOHHLA
LNRDLITSSVEKDSGGKTPGDFNYAYQKPENAAGSPDEEDX DYESQEKTIRTHVYNY
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Lien,L.L., Feener,C., Fischbach,N. and Kunkel,L.M.
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/product-"microtubule-associated protein 18"
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Best Local Similarity 73.9%; Pred. No. 1.34e+00;
Matches 34; Conservative 0; Mismatches 12; Indels
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EEEYEPEKMEAEDYVWAVVDKAAEAGGAEEOYGFLTTPTKOLGAGSFGREPASSIHDE
TLPGGSESEATASDEBNREDQPEEFTATSGYTGSTIEISSEPTPMDEMGTPROVMSDE
TNNEETESPSOGEYVNITKYESSLYSOEYSKAADYTPLMGFSEGSKTDATDGKDYNASA
STISPPSSMEEDKFSRALRAYCSEVKASTTLDIKDSISAVSEKYBELSPS
PSPLEKTPLGERSVNFSLTPNEIKYGARAEVAPVSFEVTORVTGENGASPEDSTLEY
VSPSOGYTGSAGHTPYYGSPTDEKSSHLPTEVIEKPPAVPVSFEFSDAKDENERASP
PMDEVPDSESPIEKYLSPRISPLIGSESATESFLGADDKASGRAESPFEEKSGK
EDEESAKAEADAY IREKRESVASGDDRAEEDMDEAIEKGEAEQSEEEADEEDKAEDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTKTKSSSPYKKSDGKKRPLAASPKRAGLKESSDKVSRVASPKKKESVEKAAKPTTTP
EVKAARGEEKDKETKNAANASASKSAKTATAGPGTTKTTKSSAVPCLPVYLDLCY IP
NHSNSKNVDVEFFKRYRSSYYVVSGNDPAAEEPSRAVLDALLEGKAQMGSNMQVTLIP
THDSEVMREWYQETHEKQQDLNIMVLASSSTVVMQDESFPACKIEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGGKQQGRQCDETPPTSVSESAPSQTDSDVPPTTECPSTTADANIDSDDESSTIPTD
KTVTYKHMDPPPAPVQDRSPSPRHPDVSMVDPEALAIBQNLGKALKKDLKEKTIYTKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Betaherpesvirinae; Muromegalovirus.

1 (bases 1 to 13356)
Beuken,E., Slobbe,R., Bruggeman,C.A. and Vink,C.
Cloning and sequence analysis of the genes encoding DNA polymerase, glycoprotein B, ICP 18.5 and major DNA-binding protein of rat
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/db_xref="PID:g1255111"
/translation="WAEDDLANLAFVAAAAWLYLVRRDREAGEVLSVLSLCDRECPVV
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Profein, encoded by GenBank Accession Number X17403"
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Beuken, E., Slobbe, R., Bruggeman, C.A. and Vink, C.
Direct Submission
Submitted (05-MAR-1996) Cornelis Vink, Medical Microbiology, University of Limburg, PO Box 5800, Maastricht 6222 WH, The Netherlands
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Pred. No. 1.34e+00;
0; Mismatches 12; Indels (
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/organism="Rat cytomegalovirus"
/strain="Maastricht"
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Best Local Similarity 73.9%;
Matches 34; Conservative
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KEYWORDS

REFERENCE AUTHORS

TITLE

REFERENCE AUTHORS

JOURNAL

JOURNAL

TITLE

FEATURES

CDS

VSPLLIDLIVDREFVGTVRTPMSCCDDGVLTRVTSFCPFVFLFYGTEDVLSSVEDHGD VRRLCEESRRREGVRPFAPRADREPTDVAALCRRLHLDPERTLGYVACGNGLKEMLYA OEHVAALLREKILALVARGYVDFSAANILREYTRGSGGTSSSTGRRRPPVLRPVLGRG RVRLRRGRRRPLGQQRRRAVRRPRRGGGGGPGVRAGRTDDFSAVISSRGEADDAPLPO PAQRRRGRRDLPQKRGRSK"

TUTILIZE A LOIS NUTLOKLCYVCSKCNECAMDAECLKYCDPS IVLMDSTAFORNGA TVIHLYRTLYPALVAONTAQTSVLSIYLEMLLAGLYRTMRELDTALDDFARHRDRERY YRTILLIDESCPESYTLVPAGHLITIELATIMD ISLLLCKINCVSGALDBYOGYCS RLLSILGALCOTSPANAGPETYRETSTCYCYCTELMAVPNOGRS INRRIEGLLCDHYTV KKVLVQLDTDAQTVEODLGEVA IRAPRVK SITRSLKNIASSSAGSCAYINDAEBALKG YNLFSEIPERITSLSDYTWRKYESYTYRHVGVTMRQLNASHGINKALRGELSRFIYG BAVEDIFSLGEGRFAGHERWRYGS ISAAGKVTMRQLNASHGINKALRGELSRFIYG BAVEDIFSLGEGRFAGHERWRYGS ISAAGKVVDMTISMSVK SFENNDLFRILLESNE IYAKIRSLIEDIRDADDFGSTAATGTSGGTSGGTSGGTSGGTAPAGTEV PERGRRSSHGSSTSRFGTSGGTSGGTAPAGTEV GVTRGDPPEAAAASSTTAPARGNNFALECGDPLLETTHDVNKEVNVRRRAYLKKVSEVG
NVVAACITSOBHLVTRLNNNUVGTVCLEALSKVMNGFLSRQRATKEARALEPDVGES
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KYPYRICMALSTDLVRFGKTIECPAPSPKTPTEEGIMLVYKQDIVAYTFKVITYYRNL OFORSYATUMDYLLGTTVURLAMPCGEIDOINRNNGCYSTAORVMGDVYIAYHRDEE ENVYMELIPDDYVSSSSRFVSTKDAYHRRKVWMYTESCTINCVYTVTKARGNRPYS EFVLSSGERVETSPFFNGTUNDEPEEDDTANFRYBANTEMYDRFGDMNVSTHRYHRMAF LERPEYTIAMEIQNKSSALCEWKRWQVVVKARIRTAGNSSYHFVSRSLTATFVTGKHQ HNINQTRYVNCILNGTTEELDRVFEEEYNETHVKDGNVEVYOTSGGLLVFWQKTKPRR LHELGEAIWNITGENVTTESEGYNNTSRSRRRDVSSVDDIKKDITTTOLOFTYDILRD YINGALQNILEAWCLDQKRQAEMLREISKINPSNILSSIYGREVTAKLAGDVLALSEC VPVDQDSVKILKDMRIFVDNKVVNCYARPHVLFKFVNSSKIESGQLGBHNEILLGNHR TERCETPSRKIFITDEVGYBFRDYVFKNVTNLKDIELIDTMIGVSLEPLENTDFQILE LYSRGEIRASNVFNLEEIMREYNAQKQSVRFLFTOIIEDTPYLRGLDDFWGGLGAAG KGIGMVFGAVAGAVGSIASGFVSFLTNPFGTVTIIIVATVLVIYIIFRROQOAVMR PVEXFFFPHAMQVAGKPLGALGGGDDRPPSYEDSTSQGKRGNVTKGGDDAGSGHKKGSG KAYSGEDAAAMLRALQDLEESGRQAAIGVAKKVGRNILDRLRGNSGYQSLPDSDVEDR

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CDS

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Caenorhabditis elegans strain-Bristol N2.

Caenorhabditis elegans

Bukaryotaes; mitochondiala leukaryotes; Metazoa; Nematoda;

Bukaryotaes; mitochondiala leukaryotes; Metazoa; Nematoda;

Secarnentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoldea;

Rhabditidae; Caenorhabditis.

I (Bases It o 3759)

Nilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,

Bonfield, J., Button, J., Connell, M., Copsey, T., Cooper, J.,

Fulton, L., Caraton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,

Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jer, M.,

Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,

Latrellle, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,

Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopta, A.,

Staden, R., Sulston, J., Thierry-Mieq, J., Thomas, K., Vaudin, M.,

Valdhan, K., Waterston, R., Smaldon, N., Weinstock, L.,

Valkinson-Stroat, J. and Wohldman, P.,

Nilkinson-Stroat, J., A.,

Nilkinson-Stroat, J., and Wohldman, P.,

Nilkinson-Stroat, J., A.,

Nilkinson-Stroat, J.,

Ni
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VREAKIPIHAEKYFDQIVKAVTNVLLPVFPKDMPRRERFFAYVLPIRTYLPEVFLRMS
KEDRECGAYLARESGLGMNSFIVYGEDTCGTG"
                                    ATGLIKTQCELSPRMFFEDREYVLDPVMVWPGLDIAADGEAVPPCDFVFHTFDQVVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6117 aaaggtttccgaggtgggctacaacaaggttatggcctgcatcaagagccaggagcac 6174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 AAACGITICCIGGGIGGICCACTIAAIGGAGAIGICCAGAAACACGAGCGAGCAGCAC 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELKOSB2 37599 bp DNA
Caenorhabditis elegans cosmid KOSB2.
UZ9379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUN-1995)
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Chissoe, S.
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3 (bases 1 to 37599)
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Best Local Similarity 69.0%;
Matches 40; Conservative
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DEFINITION

LOCUS

g G Cp ACCESSION

KEYWORDS

ORGANISM

REFERENCE AUTHORS

SE COUNT

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e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
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NEIGHBORING COSMID INFORMATION:
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The 5' cosmid is T07F12, 500bp overlap; 3' cosmid is ZK389. Actual start is at base position 1 of CELK05B2; actual end is at base position 37599 of CELK05B2.
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Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green and L. Hillier, ms in preparation).

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PENDLMKKLENEKKODENGDENGENEEVETSFDLGGGGTSTPLIVLYA."

COMPLEMENT(1010,11621..11659,11721..11996,1255..1244,
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                                                                                                                                                         /organism-"Caenorhabditis elegans"
Location/Qualifiers
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                           FEATURES
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> REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

TITLE

TITLE JOURNAL

COMMENT

AUTHORS

REFERENCE

CDS

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22113..22238,22286..22483,22536..22762,23207..23460,
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25836..25940,26403..26437,28217..28299))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22; DB 37; Length 37599;
Pred. No. 1.34e+00;
0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6467 g 12316 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6692 aaaattaattagaatcaaggaaagtgaaatag 6723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 AAAATTAATTAGGATCATGCAAAGTCAGATAG 451
                                                                                                                                                                                                                                            /codon_start=1
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Best Local Similarity 84.4%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6305 c
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Search completed: Tue Dec 2 17:04:37 1997 Job time : 437 secs.

US-08-915-004-10.rst2

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	(AE)
	2.1D John F. Collins, Biocomputing Research Unit. ht (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a.	- n.a. database search, using Smith-Waterman algorithm
Run on: ular output no	Tue Dec 2 16:51:33 1997; MasPar time 315.17 Seconds 949.537 Million cell updates/sec not generated.
Title: Description:	>US-08-915-004-10 (1-1089) from US08915004.seq
Periect score: N.A. Sequence: Comp:	1089 1 ATGAACAAGTTGCTGTGCTGTAAAAATAAGCTGCTTATAA 1089 TACTTGTTCAACGACACGACATTTTTATTCGACGATATT
Scoring table:	TABLE default Gap 6
Nmatch STD:	Dbase 0; Query 0
Searched:	359085 segs, 137405154 bases x 2
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	3:EST201 4:EST202 5:EST203 6:9:EST207 10:EST208 11:EST20 112 15:EST213 16:EST214 17:ES 17 20:EST218 21:EST219 22:ES 22 25:EST223 26:EST224 27:ES 27 30:EST228 31:EST229 32:ES
atabase:):STS5 41:STS6 42:ST: [7:STS12 48:STS13
	49:qneST1 50:qneST2 51:qneST3 52:qneST4 53:qneST5 54:qneST6 55:qneST7 56:qneST8 57:qneST9 58:qneST10 59:qneST11 60:qneST12 61:qneST13 62:qneST14 63:qneST15

64:gnESTI6 65:gnESTI7 66:gnESTI8 67:gnESTI9 68:gnEST20 69:gnEST20 69:gnEST21 70:gnEST22 72:gnEST23 72:gnEST24 73:gnEST25 74:gnEST25 74:gnEST2 77:enEST3 72:gnEST4 78:gnEST25 74:gnEST2 80:enEST1 76:enEST3 82:enEST8 83:enEST4 84:enEST10 85:enEST10 86:enEST12 87:enEST18 88:enEST14 89:enEST10 85:enEST10 86:enEST10 87:enEST10 87:enEST

Mean 11.077; Variance 1.866; scale 5.938 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query

Result

WashU-Merck EST Project Washington University School of Medicine

NO. SO. SO. SO. SO. SO. SO. SO. SO. SO. S

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/note="forging marging for the property of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -28ml3 rev2 FT from Amersham High quality sequence stop: 448.
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Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevaškis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
"The washU-Merck EST Project";
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Contact: Wilson RK WashU-Merck EST Project Washington University
School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
Forest Park Parkway, Box 8501, St. Louis, MO 63108
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06-MAR-1997 (Rel. 51, Created)
06-MAR-1997 (Rel. 51, Last updated, Version 1)
2147908.rl Soares NhHMPu S1 Homo sapiens cDNA clone 666590 5'
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Eukariyotae; mitochondrial eukaryotes; Metazoa; Chordata;
Verteprata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.00e+00;
0; Mismatches 1; Indels (
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                                                                Email: est@watson.wustl.edu
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1 Similarity 99.5%;
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Fax: 314 286 1810
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte ZNDHM, pregnant uterus NDHPU, and fetal heart NDHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction
                                                                                                                                                                                                                                                                                                                                                        The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484688-489479.
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zr3503.rl Soares NhHMPu Sl Homo sapiens cDNA clone 665356 5'.
AA195113
91784803
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Socres,M., Tan,F., Treyaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
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MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 448.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 0.00e+00;
0; Mismatches 1; Indels C
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WashU-Merck EST Project
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221; Conservative
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PCR Profile:
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                                                                                                                                                      /organism="Homo sapiens"
/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT713D-Pac
/note="Organ: mixed (see below); Vector: site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NDHM, pregnant uterus
NDHPU, and fetal heart NDHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was FCR-amplified CDNAs from pools 5,000 clones made from the same 3 libraries. The pools
340488-345479, and 484488-489479."
//lone="665556"
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Location/Qualifiers
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Location/Qualifiers
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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/note="Organ: mixed (see below); Vector: pl7l3D-Pac
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Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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WashU-Merck EST Project
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Best Local Similarity 100.0%;
Matches 74; Conservative
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JOURNAL
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(Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECC RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 444488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STS sequence; primer; sequence tagged site.
human Plasmid clones, generated from a lymphoblastoid cell line
human male. Localized to human chromosome 12 by analysis on
the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell
Institue for Medical Research, Camden, NJ 08103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygli; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
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                                                                                                                                                                                                                                                                                                       /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus" /lab_host="DH10B"
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62 degrees C for 23 seconds
72 degrees C for 30 seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tal: 4157259687
Pax: 4157259689
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O
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Pred. No. 6.00e-105;
0; Mismatches 0; Indels
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Perkin Elmer 9600
                                                                                                                                                                                                                                                                                               /clone_lib="Soares NhHMPu S1"
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Primer B: TGGTGGGGAGTATCAGGTTC
STS size: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini; Hominidae; Homo.

1 (bases 1 to 400)
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Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermal Cycler:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.8%;
Best Local Similarity 100.0%;
Matches 74; Conservative
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Terrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
1 (bases 1 to 245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prepared with primer pairs derived from random genomic sequence.
                                                                                                                                                                                                                                                                                                                                                          Whitehead Institute/MIT Center for Genome Research; Physically Mapped SISs
                                                                                                                        23-0CT-1995
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/map="791_B-4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;
963_G_6"
a 28 c 35 g 87 t 3 others
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56.155
/map="791.B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;
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Pred. No. 1.84e-03;
0; Mismatches 14; Indels
                                                                                                                      STS
                                                                                                                                                                                      SIS sequence; primer; sequence tagged site. human SISs derived from random genomic DNA.
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Annealing: 56 degrees C
POlymerization:
PCR Cycles: 35
Thermal Cycler:
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Primer: each 5 pM
dNTPs: each 4 nM
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MgCl2: 1.5 mM
KCl: 50 mM
Tris, 4cl: 10 mM
                                                                                                            245 bp
human STS MR4116.
G11923
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Best Local Similarity 70.8%;
Matches 34; Conservative
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                                                                                                                                DEFINITION
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                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant physiol. 106:1241-1255(1994).
AGIS: 742477; AGIS July 1995.
Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, Mi Tel: 517.353-0854 Fax: 517-353-9168
Email: 22313tcn@lbm.cl.msu.edu. NCBI gi: 933235
Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 400;
                                                                                                                                                                                                                                                                                                                                                                                        6 others
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Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
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2.0%; Score 22; DB 77; Length 472;
Local Similarity 68.6%; Pred. No. 9.42e-05;
nes | 35; Conservative 0; Mismatches 16; Indels
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0; Mismatches 6; Indels
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/clone="113K157"
/strain="var columbia"
/note="thale cress"
Sequence 472 BP; 126 A; 97 C; 100 G; 137 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-1995 (Rel. 42, Created)
12-MAR-1997 (Rel. 51, Last updated, Version 15)
5740 Arabidopsis thaliana cDNA clone 113K15T7.
    each 200 uM
0.05 units/ul
10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22; DB 39;
Pred. No. 9.42e-05
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                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                2.5 mM
50 mM
20 mM
8.3
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                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  63 g
dNTPs:
Taq Polymerase: (
Total Vol:
                                                                                                                                                                                          Chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.4%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                    230..250
/map="12"
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230..250
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                                                                                              MgC12:
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MEDLINE; 95148729.
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T42477;
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LOCUS 103759 392 bp mRNA EST 14-FEB-1997
DEFINITION IB862 Infant brain, Bento Soares Homo sapiens cDNA clone IB862
ACCESSION T03759
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project washu-HHMI Mouse EST Project washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wistl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llhi.gov) for further information. MGI:217450 Seq primer: mob.REGA+ET.
 Gaps
                                                                                                                                                                                                                                                                                                                                    Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Moris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
                                                                                                                                                                  04-MAY-1996 (Rel. 47, Created)
05-WARR-1997 (Rel. 51, Last updated, Version 2)
mb83g02.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 336050
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                                                                                                                                                                                                                                             --- musculus (house mouse)
Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minoru KO (Wayne State University)."
/clone="336050"
/clone_lib="soares mouse p3NMF19.5"
/clone_lib="soares" l19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA <1..>377
Sequence 377 BP; 109 A; 85 C; 94 G; 89 T; 0 other;
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@
                                123 acacageteacatgtacagacaataaaaetgeteaag 159
                                                      729 ACACAGCTCACAAGAACAGACTTTCCAGCTGCTGAAG 765
      0; Mismatches
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                                                                                                                          standard; RNA; EST; 377 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.; "The WashU-HHMI Mouse EST Project";
        29; Conservative
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                                                                                                                 MM05110
W18051;
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/map="923_H_8; 959_F_5; 441.7 cR from top of Chrl7 linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="923_H_8; 959_F_5; 441.7 cR from top of Chr17 linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29..253
/map="923_H_8; 959_F_5; 441.7 cR from top of Chr17 linkage
                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda, Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                       Whitehead Institute/MIT Center for Genome Research; Physically
                                                                                                        19-0CT-1995
                                                                                                                                                                     STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prepared with primer pairs derived from 238433 -- dbEST. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 others
                                                                                                                                                                                                                                                                                                                                                                                                 Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research 9 Cambridge Center, Cambridge NA 02142 USA
                Score 21; DB 38; 1 Pred. No. 1.84e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACAGTIGIGAAGCCGIGC
225
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Primer: each 5 pM
dNTPS: each 4 nM
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Thomas Hudson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.9%;
Best Local Similarity 78.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total Vol: 20 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 c
                                                                                                             GU6067 253 bp
human STS WI-6406.
                                                                                                                                                                                                                                                                                                                                                              Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 617 252 1900
Fax: 617 252 1902
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PCR Profile:
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                                                                                                                                                                                                            collection.
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                                                                                                                                    DEFINITION
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                                                                                                                                                   ACCESSION
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                                                                                                                                                                                                   SOURCE
                                                                                                       RESULT
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ORGANISM

REFERENCE

JOURNAL

COMMENT

TITLE

FEATURES

NID KEYWORDS

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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                           double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand possible reversed clone: similarity on wrong strand seq primer: -41ml3 fwd. ET from Amersham.

Location/Qualifiers
                                                                                                                                                                                                            /note="Vector: pBluescript SK-; Site_1: EcoR1; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dr. Pool
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION mw82b02.rl Soares mouse NML Mus musculus cDNA clone 677163 5.

REMANDER

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WashD-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.9%; Score 21; DB 24; Length 431
Best Local Similarity 71.7%; Pred. No. 1.84e-03;
Matches 33; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 gcaaggaaatgcagtattttatgcagcagtggactgntaccaacaa 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 GCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAA 305
                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                              113 t
                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                        /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                       93 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 286 1800
314 286 1810
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                                                                                                                                                                   Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
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JOURNAL
                                                                                                                                         FEATURES
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                                    Eukaryotae, mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthbria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 392)
Rhan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Stevens, T.J., Robinson, M., Orpana, A.K. and Sikela, J.M. Single pass sequencing and physical and genetic mapping of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/note="Vector: BA, M13-derived; Site_1: HindIII; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zq16e09.sl Stratagene fetal retina 937202 Homo sapiens cDNA clone PROTEIN 1B. ;
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Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata;
Usases 1 to 431)
Hiller,L. Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollan,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Farsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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WashU-Morck EST Project
Washington University School of Medicine
TH4 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                    Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
Email: nikki@tally.uchsc.edu
Seq primer: -21M13 Universal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Infant brain, Bento Soares"
/lab_host="E. coli DH5-alpha"
complement(<1..>392)
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Pred. No. 1.84e-03;
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                                                                                                                                                                                                  Nature Genet. 2, 180-185 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Similarity 78.4%;
                                                                                                                                                                                                                                                                   Contact: Sikela JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 C
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                   Homo sapiens
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91833137
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Query Match Best Local

Matches

BASE COUNT

ORIGIN

mRNA

naman.

ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE COMMENT

ACCESSION

KEYWORDS

LT 11 DEFINITION

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RESULT
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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     constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA213094 443 bp mRNA EST 31-JAN-1997
mw82b02.rl Soares mouse NML Mus musculus cDNA clone 677163 5',
AA213094
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                                                                                                                                                                                                                                                                                                  Gaps
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1.84e-03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                            Length 443;
                                                                                                                                                                                                                                  Score 21; DB 60; Lenguary...
Pred. No. 1.84e-03;
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Location/Qualifiers
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/clone_lib="Soares mouse NML"
/lab_host="DH10B"
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                                                                       /clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
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Unpublished (1996)
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library constructed and normalized by Bento Soares and M.Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Enail: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL.; contact the IMAGE Consortium (info@image.lnl.gov) for further information. MGI:416867 Seq primer: -28m13 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Gelsel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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20.FEB-1997 (Rel. 51, Last updated, Version 2)
mw82b02.rl Soares mouse NML Mus musculus cDNA clone 677163 5'.
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Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
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Best Local Similarity 88.9%; Pred. No. 1.84e-03;
Matches 24; Conservative 0; Mismatches 3; Indels
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Sequence 443 BP; 123 A; 105 C; 118 G; 97 T; 0 other;
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12-MAR-1997 (Rel. 51, Last updated, Version 9)
21953 Arabidopsis thaliana cDNA clone G8G4T7.
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MMAA13451 standard; RNA; EST; 443 BP.
AA213094:
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RA MEDLINE; Oblingge J., Green P., Keegstra K., Kende H., Retzel E., Somerville C.,
RA Retzel E., Somerville C.,
RT Grees galore: a summary of methods for accessing results from RT large-scale partial sequencing of anonymous Arabidopsis cDNA RL Lones;
R. Langers;
C. Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan C. Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan C. State University MSU-DOE PRL, MIchigan State University, Plant C. Email: 22313tcn@thom.cl.msu.edu. NOEI gi: 1269126
F. Key
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Best Local Similarity 80.0%; Pred. No. 1.84e-03;
Matches 28; Conservative 0; Mismatches 7; Indels
 Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                         /Organism="Arabidopsis thaliana"
/clone="GBG477"
/strain="var columbia"
/note="thale cress"
/note="thale cress"
/l.>496 BP; 132 A; 87 C; 124 G; 137 T; 16 other;
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Search completed: Tue Dec 2 16:56:58 1997 Job time : | 325 secs.

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TACTTGTTCAACGACACGAC.....ATTTTTATTCGACGAGAATATT
                                                                       | 1.EST1 2.EST2 3.EST3 4.EST4 5.EST5 6.EST6 7.EST7 8.EST8 |
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| 1.EST15 10.EST10 11.EST17 12.EST12 13.EST13 14.EST14 |
| 2.EST21 22.EST22 23.EST23 24.EST24 25.EST25 26.EST26 27.EST27 28.EST38 39.EST33 33.EST33 34.EST34 34.EST34 34.EST34 34.EST34 45.EST36 37.EST37 38.EST38 39.EST39 40.EST40 41.EST41 42.EST42 43.EST43 44.EST44 45.EST45 46.EST46 47.EST47 48.EST48 49.EST49 44.EST44 44.EST44 45.EST57 58.EST57 58.EST55 56.EST56 57.EST57 58.EST57 58.EST57 56.EST56 65.EST66 61.EST61 62.EST66 63.EST66 64.EST64 65.EST64 65.EST66 66.EST66 61.EST67 61.EST70 71.EST77 77.EST77 77.EST77 77.EST77 74.EST77 74.EST74 74.EST74 75.EST75 76.EST76 77.EST77 78.EST78 79.EST79 80.EST86 87.EST99 84.EST89 89.EST99 90.EST99 91.EST99 91.EST99 92.EST99 93.EST99 94.EST99 94.EST99 94.EST90 91.EST91 92.EST99 93.EST199 94.EST10 101.EST101 102.EST107 108.EST103 104.EST104 115.EST110 116.EST110 117.EST111 113.EST113 114.EST119 116.EST110 116.EST116 117.EST117 118.EST113 114.EST119 116.EST116 116.EST116 117.EST117 118.EST113 114.EST114 115.EST115 116.EST116 117.EST117 118.EST118 139.EST13 134.EST13 135.EST13 136.EST13 136.EST16 156.EST16 16.EST16 17.EST117 18.EST118 139.EST13 136.EST16 16.EST16 16.EST16 17.EST117 18.EST118 139.EST13 136.EST13 13
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                                                                                                                                       Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.
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- (1-1089) from US08915004.seq
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Listing first 45 summaries
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175:EST175 176:EST176 177:EST177 178:EST178 179:EST179 180:EST180 181:EST181 182:EST182 183:EST183 184:EST184 185:EST185 186:EST181 187:EST183 184:EST189 185:EST185 186:EST189 197:EST190 197:EST197 198:EST198
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Statistics: Mean 11.043; Variance 1.850; scale 5.968

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No	0.00e+	.39e-0 1.45e-	45e-04	.45e-	1.45e-0	4 5 6 - U	1.400	.45e-0	5e-0	1.45e-	2.90e-0	0-906	.90e-u	0-906.7	0-406	.90e-0	90e-0	.90e-03	5.90e-	2.90e-0	0-e06	.90e-03	2.90e-	90e-03	2.90e-	2.90e-0	2.90e-0	2 90e-0	2.90e-0	2.90e-0	2.90e-0	2.90e-0	2.90e-03	2.90e-	2.90e-0	2.90e-0	2.90e-0	2000	900	. שטעי
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ALIGNMENTS

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ESSION	AA037313								
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                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1203 Std Bror: 0.00 Seq primer: -28413 rev2 from Amersham High quality sequence stop: 435.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultnan,M., Kucaba,T., E.M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                        WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 394; DB 195; Length 602;
Pred. No. 0.00e+00;
0; Mismatches 0; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                      The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 36.2%;
1 Similarity 99.5%;
406; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 c
                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                          Unpublished (1995)
                  Homo sapiens
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                                                                                                                                                        Wilson, R.
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est Local S
tches 40
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JOURNAL
COMMENT
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BASE COUNT
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                                                                 REFERENCE
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                                                                                   AUTHORS
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human clone=253126 primer=M13RP1 library=Morton Fetal Cochlea vector=pBluescript SR - host=SOLR cells (kanamycin resistant) Rsitel=EcoRI Rsite2=XNoI The cDNA was oligo (dT) primed with an XhoI restriction enzyme recognition site and an 18 base poly dT sequence. For the 5' end, the synthesized cDNA termini were treated with T4 DNA polymerase and EcoRI adaptors were ligated to the blunt ends. adaptor linker: GAATTCGGCACGAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deuterostomia; Chordara, Currebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Butheria; Archoruta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 346)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Waterston,R., Williamson,A., Wohldmann,P., Trevaskis,E., WashU-Merck Est Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ym62a05.rl Homo sapiens cDNA clone 163472 5' similar to SP:S32367 H14106
ggr8954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stops: 278
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vector=p17T3D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           989 TCAGGTTCCTTCACAGCTTCACAATGTACAAATTGTATCAGAAGTTATTTTAGAAATGA 1048
                                                                                                                                                       22-NOV-1995
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Washb-Merck EST Project
Washbgton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 346;
362 cetetgtgaaaacagegtgeageggeacattgggacatgctaacetea 409
                              825 CCTCTGTGAAAACAGCGTGCAGCGCACATTGG-ACATGCTAACCTCA 871
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                                                                                                                                                    Yw23g12.rl Homo sapiens cDNA clone 253126 5'.
H88769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1049 TAGGTAACCAGGTCCAATCAGTAAAATAAGCTGCTTATAA 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 taggtaaccaggtccaatcagtaaaaataagctgcttataa 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101; DB 73; I
Pred. No. 1.35e-166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                  346 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 9.3%;
Local Similarity 100.0%;
les 101; Conservative
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Washu Merck EST Project
Washington University School of Medicine
4444 Proset Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki,T., Song,J., Koga-Ban,Y., Matsui,E., Fang,F., Higo,H., Sasaki,T., Song,J., Koga-Ban,Y., Murayama Kayano, E. et.al.
Toward cataloguing all rice genes: large-scale sequencing of randomly chosen rice cDNAs from a callus cDNA library
Plant,J. 6 (4), 615-624 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae, mitochondrial eukaryotes; Viridiplantae;
Eukaryotaa, Embryophyta group; Embryophyta; Magnoliophyta;
Charophyta,Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Oryza.
1 (bases 1 to 330)
Sasaki, T. and Minobe, Y.
Rice cDNA from callus
Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST(expressed sequence tag).
Oryza sativa (strain Nipponbare, ) callus cDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib-"Stratagene HeLa cell s3 937216"
/sex-"female"
/dev_stage="HeLa S3 cell line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22; DB 183; Length 300
Pred. No. 1.45e-04;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="SOLR (kanamycin resistant)"
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Rice cDNA, partial sequence (C0437A).
D15309
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                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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Best Local Similarity 71.2%;
Matches 37; Conservative
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Phone:0298-38-7441
Fax: 0298-38-7468
Unpublished (1995)
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AUTHORS
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                    AA100384 300 bp mRNA EST 28-OCT-1996 and 6108.rl Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 550527 5'. AA100384
                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Chordeta; Chordeta; Vertebrata; Gnathostomata; Osteichthyes; Sarcopteryqii; Choanata; Tertapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
High quality sequence stops: 313
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 300) Hilliar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                         Logaces 1 to 344)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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old male. 1st strand cDNA was primed with a Not I \mbox{\footnote{O}} ) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 344;
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Pred. No. 6.39e-06;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 GCGCCCTTGCCCTGACCACTACACAGACAGCT 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                  midbrain, pons and medulla.
Homo sapiens
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116 c 8
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Best Local Similarity 77.8%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
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Fax: 314 286 1810
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                       Gaps
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 360)
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                                                                                                                                                                                                                                                                                                                                                                                      gagtgccttggtactttaattaagaccttcaaagcttcttttctgccattcttt 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST(expressed sequence tag); Human fetal brain.
Homo sapiens fetus brain cDNA to mRNA, clone:093D09.
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                                                                                                                                                                                                                                                 Length 330;
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                                                                                                                                                                                                                                                                                                            0; Mismatches 16; Indels
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                                                                                                                                                                                                                                             2.0%; Score 22; DB 13; )
Larity 70.4%; Pred. No. 1.45e-04;
Conservative 0; Mismatches 16
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                             /organism="Oryza sativa"
/strain="Nipponbare"
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                                                                                                    /tissue_type="callus"
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                                                                                                                                 47 C
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Best Local Similarity 7
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Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 410)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV-SPORT2; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. 10.5dpc
                                                                                                                                                           WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="life Tech mouse embryo 10 5dpc 10665016"
/dev_stage="10.5dpc embryos"
/lab_host="DH10B"
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Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Heising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. Waterston, R. The WashU-HHMI Mouse EST Project
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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Pred. No. 1.45e-04;
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/clone="553259"
                                                                                                                                                                                                                                                                                                                                                 Trace considered overall poor quality Seq primer: -28M13 rev1 from Amersham High quality sequence stop: 1. Location/Qualifiers
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                                                                                                                                            Contact: Marra M/Mouse EST Project
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WashU-Merck EST Project
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Local Similarity 89.3%;
les 25; Conservative
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Gaps

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Uppublished (1995)
Other_ESTS yd72el0.s1
Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 232
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eucaryotae: Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

[ (pases 1 to 465) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                     Length 453;
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142477
9933235
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177351
g694554
Score 22; DB 111; L6
Pred. No. 1.45e-04;
                                                                                                  273 ggacacgtttcctgggtggccgctttgatgatgttgtcca 312
                                                                                                                                       74 GGAAACGTTTCCTGGGTGGTCCACTTAATGGAGATGTCCA 35
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Pred. No. 1.45e-04;
0; Mismatches 6
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Similarity 82.4%;
28; Conservative
               2.0%;
Best Local Similarity 77.5%;
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalla; Theria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: estewatson.wustl.edu
High quality sequence stops: 321
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand.
    Fax: 314 286 1810
Email: est@watson.wustl.edu
High qailty sequence stops: 212
Source: IMAGE Consortian, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N21157 453 bp mRNA EST 19-DEC-1995 yx47d01.sl Homo sapiens cDNA clone 264865 3' similar to SP:TCPB_MOUSE P80314 T-COMPLEX PROTEIN 1, BETA SUBUNIT ;.
                                                                                                                                                                                                                                                                                                            Gaps
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Washb-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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0
                                                                                                                                                                                                            9 others
                                                                                                                                                                                                                                                                      Score 22; DB 6; Length 410;
Pred. No. 1.45e-04;
0; Mismatches 7; Indels
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                                                                                                                                                                 /organism="Homo sapiens"
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57 c
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Best Local Similarity 80.6%;
Matches 29; Conservative
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Gaps

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Arabidopsis thalians
Arabidopsis thalians
Brassicaceae; Embryophyta: Magnoliophyta; Magnoliopsida; Capparales;
Brassicaceae; Arabidopsis.

1 (bases 1 to 472)

Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H.,
McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
Retzel, P. and Somerville, C.
Retzel, P.
Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half rosettes; 4) the seedlings of the light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
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Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Lillopsida; Poales; Poaceae; Oryza.
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National Institute of Agrobiological Resources
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/clone="113K157"
/strain="var columbia"
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PROJECT = 'RGP'
Submitted (14-Feb-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu.
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Best Local Similarity 68.6%;
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 0298-38-7468
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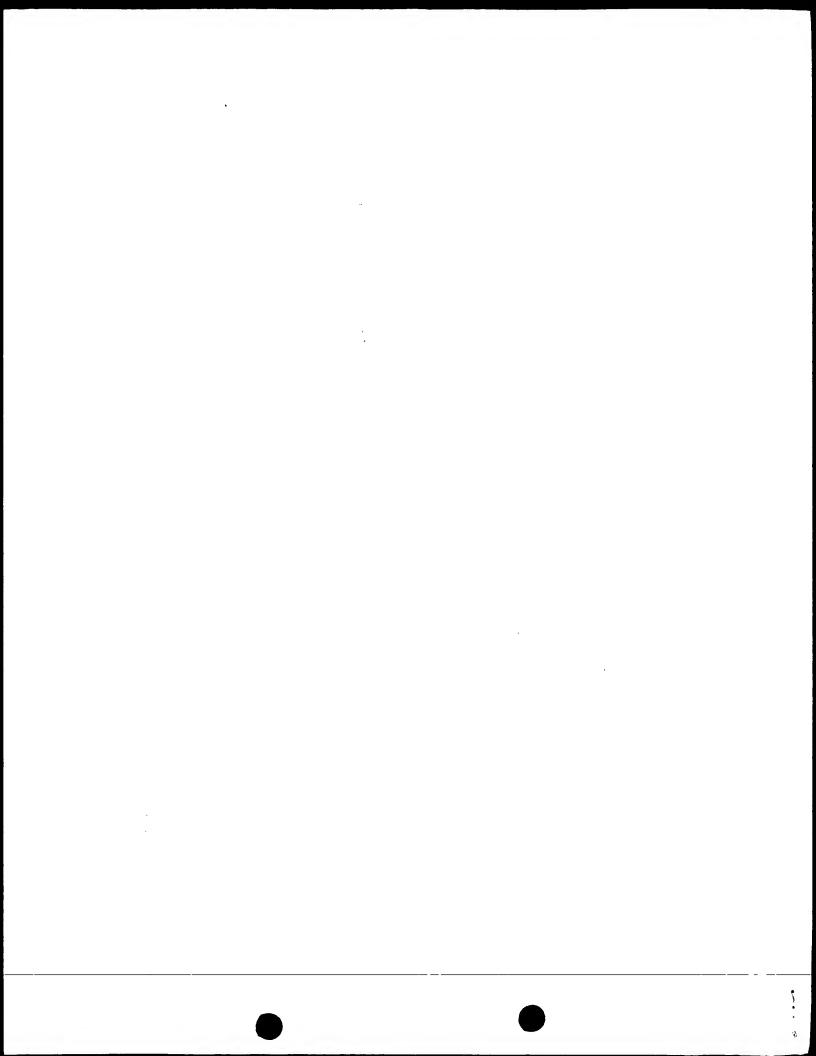
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/organism="Homo sapiens"
/organism="Homo sapiens"
/orde="Organ: eye; Vector: lambda gt10; Site_1: ECORI;
Site_2: ECORI; The library used for sequenting was a
sublibrary derived from a human retina cDNA library.
Inserts from retina cDNA library DNA were isolated,
randomly primed, PCR amplified, size-selected, and cloned
into lambda gt10. Individual plaques were arrayed and
used as templates for PCR amplification, and these PCR
products were used for sequencing."
/clone_lib=Human retina cDNA randomly primed sublibrary"
/sex=mixed (males and females)"
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55c10 Human retina cDNA randomly primed sublibrary Homo sapiens
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 796)
Macke, J., Smallwood, P. and Nathans, J.
Adult Huma Retina cDNA
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Dr. Jeremy Nathans
Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
JS North Wolfe Street, Baltimore, MD 21205
Tel: 410 955 4678
Fex: 410 614 0827
                                                                                                                                                                                                          388 cgggtgcantnacggcaaccaggtgctcaaggagctngaggaggccaagaaggngt 443
                                                                                                                                                                                                                                                     234 CGAGTGTCTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGT 289
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Pred. No. 1.45e-04;
0; Mismatches 12; Indels
                                                                                                                          Length 493;
                                                    5 others
                                                                                                                                                                   0; Mismatches 19; Indels
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/strain="Nipponbare"
/dev_stage="Green shoot (8 days old)"
. 147 c 150 g 93 t 5 otl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: CTTTTGAGCAAGITCAGCCTGGTTAAGT
BACKWARD: GAGGTGGCTTATGAGTATTCTTCCAGGGTAA
Seq primer: Location/Qualifiers
                                                                                                                        Score 22; DB 55;
Pred. No. 1.45e-04;
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/dev_stage="adult"
/lab_host="E. coli strain K802"
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Best Local Similarity 66.1%;
Matches 37; Conservative
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Best Local Similarity 73.9%;
Matches 34; Conservative
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                                                  BASE COUNT
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Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ed and directionally of the lafmid BA
                                                                                                                                                                                                                                                                                                                                                                                                              Auffray.C., Behar.G., Bois.F., Bouchier,C., da Silva,C.,
Auffray.C., Behar.G., Bois.F., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Rabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone library from B.Soares, Psychiatry Dept. Columbia University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAR-1995
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                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 253)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
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Normalization_method: Bento Soares, P.N.A.S in press;
Genexpress_library_idt: C;
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/isolate="muscular atrophy patient"
/dev_stage="3 months old"
/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
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    sapiens partial cDNA sequence; clone c-Obe06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing_method: single read, full automatic;
Primer: (-21)M13_universal;
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                                                                     partial cDNA sequence; transcribed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequence complementary to mRNA (3'end)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21; DB 129;
Pred. No. 2.90e-03;
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Direct Submission
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Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Lit, Cases I to 265)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGATTAATTAAAGATCTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pr773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
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Fax: 314 286 1810
Fax: 314 286 1810
Figh quality sequence stops: 241
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 2.90e-03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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51 c 6
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WashU-Merck EST Project
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Best Local Similarity 66.7%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                       AUTHORS
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 2 16:36:04 1997; MasPar time 121.52 Seconds 935.265 Million cell updates/sec

ular output not generated.

ltle: >US-08-915-004-10 Description: (1-1089) from US08915004.seq Perfect Score: 1089

Perfect Score: 1089

N.A. Sequence: 1 ATGAACAAGTIGCTGTGCTG......TAAAAATAAGCTGCTTATAA 1089

TACTTGTICAACGACACGAC......TATITITATICGACGAATAIT

Scoring table: TABLE default Gap 6 Searched: 142080 seqs, 52183452 bases x 2

Dbase 0; Query 0

STD

Nmatch

Post-processing: Minimum Match 0% Listing first 45 summaries Database: n-geneseq28 | i.part1 2.part2 3:part3 4:part4 5:part5 6:part6 7:part7 | 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 | 14:part14 15:part15 16:part16 17:part17 18:part18 | 19:part19 20:part20 21:part21 22:part22 23:part23 | 24:part24 25:part25 26:part26 27:part27 28:part28

Statistics: Mean 9.038; Variance 4.941; scale 1.829

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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RESULT 1

D 73475 standard; cDNA; 1173 BP.

AC 735475

DE Munaut mecrosis factor receptor: TNF-beta; ligand; tumour;

M differentiation; immune response; autoimmune disease; inflammation;

KW differentiation; immune response; autoimmune disease; inflammation;

KW differentiation; immune response; succimmune disease; inflammation;

KW septic shock; graft-versus-host; apoptosis; ss.

HW W Saples.

Cocation/Qualifiers

FT /*tag b 1..133

FT /*tag b 1..1173

FT /*ta
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Query Match

80.0%; Score 871; DB 28; Length 1173;

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Mutated OCIF, OCIF-CSph, coding sequence.
Ostepclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
Synthetic.
Location/Qualifiers
                                                                                                                                                61 CAGGAAACGITICCICCAAAGIACCIICATAIGACGAAGAAACCICICAICAGCAGIAG 120
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1 Similarity 100.0%;
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PT DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 81; Page 169; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CSph in which amino acids 298-380 of the mature protein have been deleted and replaced by Ser-Leu-Asp. These amino acid changes have been caused by the introduction of a restriction site. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 Kb under reducing conditions and 120 kD under non-reducing conditions. The protein is adoorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 50 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and control of bone resorption and therefore in the treatment and sequence 966 BP; 301 A; 228 C; 226 G; 211 T;
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Yasuda H;
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29-AUG-1996.
20-EEB-1996; JP-054977.
21-ULL-1995; JP-207568.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochizuki f
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1..63
                                                                                 OCIF-CSph
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P-PSDB; R99949
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This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CC in which amino acids 331-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 6 Nb under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Sequence 1056 BP; 332 A; 252 C; 247 G; 225 T;
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20-FEB-1995; JP-05497.
21-07B-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(SOLOW ) Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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larity 99.9%; :
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22-APR-1997 (first entry)
Mutated OCIF, OCIF-CBst, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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121 tgtgacaaatgtcctcctggtacctacctaaaacaacactgtacagcaaagtggaagacc
                   cataggagctgcctcctggatttggagtggtgcaagctggaacccagagcgaataca
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                                                                     gtgtgcgccccttgccctgaccactactacacagacagctggcacaccagtgacgagtgt
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T33178 standard; DNA; 1182 BP
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20-FEB-1995; JP-054977.
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                                                                                                                                                                                                                                                                                                                                                                          Score 869; DB 27; Length 1182; Pred. No. 0.00e+00;
21-JUL-1995, JP-207508.

(SNOW ) SNOW BRAND MILK PROD CO LTD.

(SOCO M. Higashio K, Kobayashi F, Mochizuki S, Morinaga T Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H; WPI; 96-402320/40.

P-PSDB: R99948.

DNA encoding osteoclastogenesis inhibitory factor protein for bone resorption control, esp. treatment of osteoporosis claim 78; Page 148; 183pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Mutated OCIF, OCIF-CL, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
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29-AUG-1996; J00374.
20-AUG-1995; JP-034977.
PR 21-JUL-1995; JP-207508.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
T GOLD M, Higgshio K, Kobaysshi F, Mochizuki S, Morando M, Shima N, Tsuda E, Ueda M, Yano K, Yano M, Andrew M, Shima N, Tsuda E, Ueda M, Hano K, Yano M, Andrew M, Shima N, Tsuda E, Ueda M, Hano K, Yano M, Shima M, Shima M, Tsuda E, Ueda M, Hano K, Yano M, Shima M, Shima M, Tsuda E, Ueda M, Hano K, Yano M, Shima M, Shima M, Tsuda E, Ueda M, Hano K, Yano M, Shima M, Shima M, Tsuda E, Ueda M, Hano K, Yano M, Shima M, Shima M, Tsuda E, Ueda M, Hano K, Yano M, Shima M, Shima M, Tsuda E, Ueda M, Hano K, Yano M, Shima M, Tsuda E, Ueda M, Hano K, Yano M, Shima M, Shima M, Tsuda E, Ueda M, Hano M, Shima M, Shima M, Tsuda E, Ueda M, Hano M, Shima 
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T33172 standard; DNA; 1200 BP.
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05teoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
 cataggagctgccctcctggatttggagtggtgcaagctggaaccccagagcgaaataca
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                                                                        301 CACAACCGCGTGTGCGAATGCAAGGAGGCGCTACCTTGAGATAGAGTTCTGCTTGAAA
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a M, Yano
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LT'GOROW ) NOW BRAND MILK PROD CO LT'GOROW NA SAMAN N, Shima N, Tsuda E, UGWPI: 96-402320/40.
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This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C22S in which the 22nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
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                                                                                                                                                           389 A;
                                                                                                                                                                                    tch 79.8%;
al Similarity 99.9%;
870; Conservative
                                                                                                                                                           1206 BP;
                                                                                                                                             osteoporosis
                                                                                                                                                           Sequence
                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                    22-APR-1997 (first entry)
Ostebolastogenesis inhibitory factor coding sequence.
Ostebolastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OUIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atgaacaacttgctgtgctgcgcgctcgtgttttctggacatctccattaagtggaccacc 60
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Yasuda H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding osteoclastogenesis inhibitory factor protein for bone resorption control, esp. treatment of osteoporosis Claim 8; Page 66-67; 183pp; Japanese.
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29-AuG-1996.
F 20-FEB-1996. J00374.
PR 20-FEB-1995. JP-054977.
PR 21-JuL-1995. JP-207508.
PA (SNOW PRAND MILK PROD CO LTD.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
TOWN N. Shima N. Kobayashi F. Mochizuki S. Mori
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  841 gtgcagcggcacattggacatgctaacctca
                          841 GIGCAGCGCACATTGGACATGCTAACCTCA
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T36685 standard; DNA; 1206 BP
T36685;
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WO9626217-A1.
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 39; Page 136-137; 183pp; Japanese This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C23S in which the 23rd Oys residue in the mature oCIF protein is substituted by Ser. The OCIF of the invention has molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore
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Mutated OCIF, OCIF-C23S, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
361 CATAGGAGCTGCCCTCCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACA 420
                                                                                                                                                                                                                                                                                                                                 600
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                                                                                                                                                                                                                                                                                                                                                                                                   541 CACGACAACATATGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACC
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                                                              gtttgcaaaagatgtccagatgggttcttctcaaatgagacgtcatctaaagcaccctgt
                                                                                                                               421 GTTTGCAAAAGATGTCCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGT
                                                                                                                                                                                                                                                                                                                                        cacgacaacatatgttccggaaacagtgaatcaactcaaaaatgtggaatagatgttacc
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Yasuda H;
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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WO9626217-A1.
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P-PSDB; R99935
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Mutated OCIF, OCIF-C20S, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aaacggcaacacagctcacaagaacagactttccagctgctgaagttatggaaacatcaa 780
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                                                                                                                                   61 caggaaacgitticciccaaagtaccitcattaigacgaagaaaccictcatcagcigitg 120
                                                                            1 atgaacaacttgctgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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0
                         Length 1206;
                                                   2; Indels
268 G;
                         Score 867; DB 27;
Pred. No. 0.00e+00;
                                                     0; Mismatches
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285 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T33162 standard; DNA; 1206 BP T33162;
389 A;
                        Query Match
Best Local Similarity 99.8%;
Matches 869; Conservative
1206 BP;
  Seguence
                           Query Match
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 30; Page 133-134; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C20S in which the 20th Cys residue in the mature ociF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the present and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtttgcaaagatgtccagatggttcttctcaaatgagacgtcatctaaagcaccctgt 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.4%; Score 865; DB 28; Length 1206; Best Local Similarity 99.7%; Pred. No. 0.00e+00; Matches 868; Conservative 0; Mismatches 3; Indels 0;
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a N, Shima N, Tsuda E, Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 C;
                                                                                                                                                                                                                                                                                                                 20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F,
                                                             Location/Qualifiers
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P-PSDB; R99932.
osteoporosis; ss.
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Programmer of the property of 
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                    ctgagtgaggaggatttttcaggtttgctgttcctacaaagtttacgcctaactggctt
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W09626217-A1.
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22-APR-1997 (1
Mutated OCIF, C
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T33161, 22-APR-1997 (first entry)
Mutated OCIF, OCIF-C195, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;

Location/Qualifiers 1..63

osteoporosis; ss.

/*tag= b /product= OCIF-C19S WO9626217-A1.

/*tag= a mat_peptide sig_peptide Synthetic.

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Franch Assays.

DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 27; Page 132; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C19S in which the 19th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                                Morinaga I
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 G;
                                                                                                Mochizuki
a M, Yano
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29-AUG-1996.
20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochiz
NP1: 96-402320/40.
P-PSDB; R99931.
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for bone rescription control, esp. treatment of osteoporosis Claim 57; Page 142-143; 183pp; Japanese.
This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DDD2 in which amino acids 233-326 of the mature protein have been deleted. The OCIF of the invention has a molecular protein have been deleted. The OCIF of the invention has a molecular non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 in the control of bone resorption and the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. Sequence 984 BP; 313 A; 236 C; 212 G; 223 T;
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Mutated OCIF, OCIF-DDD2, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
aacaaagaccaagatatagtcaagaagatcatccaagatattgacctctgtgaaaacagc 840
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                                                                                                                                         Morinaga T;
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F, Mochizuki S,
Ueda M, Yano K,
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20.FEB-1995; JP-054977.
21.UL-1995; JP-207508.
SINW J SNOW BRAND MILK PROD CO LTIC
GOCO M, H19SANIO K, KODBASANI F,
ARKAGAWA N, SNIMA N, TSUGA E, UGG
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T33171 standard; DNA; 984 BP.
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Local Similarity 99.9%;
Les 817; Conservative
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/product= OCIF-DDD2
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P-PSDB; R99941.
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mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-1997 (first entry)
Mutated OCIF, OCIF-CDD2, coding sequence.
Osteochlastogenesis inhibitory factor; OCIF; heparin; bone resorption;
cataggagctgccctcctggatttggagtggtgcaagctggaaccccagagcgaaataca
                                            ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc
                                                                                                                            CACAACCGCGTGTGCGAATGCAAGGAAGGCGCTACCTTGAGATAGAGTTCTGCTTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA epcoding osteoclastogenesis inhibitory factor protein - for bone resorption control, esp. treatment of osteoporosis Claim 65; Page 145; 183pp; Japanese.
This Sequence encodes a mutated version of the full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yasuda H;
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a M, Yano K,
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Nakagawa N, Shima N, Tsuda E, Ueda M,
WPI; 96-402320/40.
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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WO9626217-A1.
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P-PSDB; R99944
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sequence encodes OCIF-CDD2 in which amino acids 252-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of Go kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Pred. No. 0.00e+00;
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Best Local Similarity 99.9%;
Matches 815; Conservative
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                                                                                                                                                                                                                                                                              DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 42; Page 137-138; 183pp; Japanese.

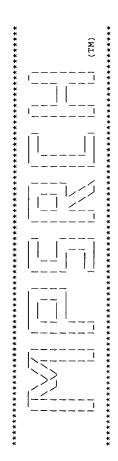
This sequence encodes mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DCR1 in which amino acids 2-42 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.

Sequence 1083 BP; 352 A; 250 C; 246 G; 235 T;
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          22-APR-1997 (first entry)
Mutated ocIF: OcIF-DCR1, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
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21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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Pred. No. 0.00e+00;
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                                                                          Location/Qualifiers 1..63
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Local Similarity 100.0%;
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20-FEB-1996; J00374
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for bone resorption control, esp. treatment of osteoporosis
Claim 54; Page 141-142; 183pp; Japanese.

This sequence encodes a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence encodes OCIF-DDD1 in which amino acids 178-252 of the mature
protein have been deleted. The OCIF of the invention has a molecular
weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under
non-reducing conditions. The protein is adsorbed onto cation-exchangers
or heparin and its activity is lowered after 10 mins at 70 deg.C or 30
mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful
in the control of bone resorption and therefore in the treatment and
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Mutated OCIF: OCIF-DDD1, coding sequence.
OSteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 atgaacacttgctgtgctgcgcgctcgtgttctggacatctccattaagtggaccacc 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding osteoclastogenesis inhibitory factor protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CAGGAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TGTGACAAATGTCCTCCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGGCC
gtagacaatttgcctggcaccaaagtaaacgcagagagtgtagagaggataaaacggcaa
                                                                                                                                    cacageteacaagaacagaettteeagetgetgaagttatggaaacateaaaacaaagae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 184.9%; Score 598; DB 27; Length 981; Similarity 99.2%; Pred. No. 0.00e+00; Conservative 0; Mismatches 5; Indels
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F, Mochizuki S,
Ueda M, Yano K,
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20-FEB-1995; JP-054977.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higgashio K, Robayashi F, Makagawa N, Shima N, Tsuda E, Ueda WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       727 cacattggacatgctaacctca 748
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T33170 standard; DNA; 981 BP.
T33170;
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regaccactactors regaccacagagactgca regaccagagactgcaccaccaccaccaccaccaccaccaccaccaccaccac		181		agtacgtcaagcaggagtgcaatcgcacc 300		egotaccitgagatagagttctgcttgaaa 360		ytgcaagctggaaccccagagcgaaataca 420	STGCAAGCTGGAACCCCAGAGCGAAATACA 420	ccaaatgagacgtcatctaaagcaccctgt 480	CAAATGAGACGTCATCTAAAGCACCCTGT 480	tcctgctaactcagaaaggaaatgcaaca 540	TCCTGCTAACTCAGAAAGGAAATGCAACA 540	ccaactcaaaaatgtggaatagatattgac 600	CAACTCAAAAATGTGGAATAGATGTTACC 600		2.	
				; dtgcaaggagctgcagtacgtcaagcagga	STGTGCAAGGAGCTGCAGTACGTCAAGCAGGA	gatgcaaggaagggcgctaccttgagataga		cctggatttggagtggtgcaagctggaaccc	CTGGATTTGGAGTGGTGCAAGCTGGAACCCC	:cagatgggttctctcaaatgagacgtcatc	CAGATGGGTTCTTCTCAAATGAGACGTCATC	gcagtgtctttggtctcctgctaactcagaa		ccggaaacagtgaatcaactcaaaatgtgg	CACGACAACATGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACC		2 16.40.26 1997	



protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Dec 3 10:06:20 1997; MasPar time 2.51 Seconds 29.342 Million cell updates/sec Run on:

bular output not generated.

>US-08-915-004-1 (1-6) from US08915004.pep 47 Description: Perfect Score: :e:

1 XYHFPK 6 PAM 150 Gap 15 Scoring table: Sequence:

101610 segs, 12294212 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq28 Database:

liparti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21

Mean 14.688; Variance 38.315; scale 0.383 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	6.35e+01	8.43e+01	1.47e+02	1.47e + 02
Description	Osteoclastogenesis in	Mutated OCIF, OCIF-DD	OCIF,	OCIF,	Mutated OCIF, OCIF-DC	Mutated OCIF, OCIF-DC	Mature osteoclastogen	Mutated OCIF, OCIF-CB	Mutated OCIF, OCIF-CL		Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C1	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C2	Full length osteoclas	Sequence encoded by p	Tumour suppressor pro	protein, N-t	Protein transcribed f
<u>a</u>	R99921	R99940	R99939	R99937	R99938	R99936	R99924	R99948	R99942	R99935	R99932	R99931	R99934	R99933	R99925	P81265	R90766	R66461	R23005
DB	20	200	700	20	20	20	20	20	20	20	20	20	20	20	20	7	15	12	4
Length	۱۹	326	359	359	360	360	380	393	399	401	401	401	401	401	401	502	1137	188	255
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	91.5	89.4	85.1	85.1
Score	47	4 4	4 4	47	47	47	47	47	47	47	47	47	47	47	47	43	42	40	40
:1t :40.	П.	7 6	4	2	9	7	ထ	σ	10	11	12	13	14	15	16	17	18	19	20

1.47e+02 1.47e+02	1.47e+02	٠	•	1.47e+02	1.47e+02	1.47e+02	1.47e+02			1.47e+02			1.47e+02		1.47e+02	٠	4.	σ.	1.94e + 02	2.54e+02	2.54e+02	2.54e+02	2.54e+02
Human tumour necrosis Daunorubicin 14-hydro	a spi	10-11Ke		Extracellular domain	Hybrid human insulin-	Human contactin.	Human contactin (EMBL	AF-17 protein.	IGF-I receptor 957A v		IGF-I receptor 950X v	IGF-I receptor 943A v	Human IFG-1 receptor.	Human type I insulin-	<pre>IGF-1 receptor.</pre>	H	u	HTm4 protein.	Calpain large subunit	i secreted	Alteromonas hanedai l	Sequence encoded by 6	Fragment of Plasmodiu
R99357 W00729	R91277	R14402	R15048	R14403	_	22	R63759	546	R63125	R63126	R63124	R63123	R60795	R91429	R95244	R63122	R91430	W06503	R99579	W20433	R77379	R20181	R07505
20	18	~ (. 0 (· (1	m	15	1	12	Ξ	11	11	11	11	16	17	1	16	19	78	21	15	4	Н
390	2 (υ c	20.0	948	94	1018	01	9	1337	1337	1337	1337	36	1367	36	36	37	214	821	248	327	266	290
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ALIGNMENTS

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                         23-ApR-1997 (first entry)
Mutated OCIF, OCIF-DDD1.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
Osteoporosis.
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Yasuda H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 20; Length 326; Pred. No. 2.01e+01; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FBB-1996; JO0374.
20-FBB-1996; JP-054977.
21-JUL-1995; JP-207508.
(SNOW BRAND MILK PROD CO LTD.
GCto | M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 95-402320/40.
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20-FBB-1995; JO0374.
20-FBB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO |W, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; |96-402320/40.
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/noté="Mature CoIr-DDD1"
/noté="Positition of deletion, delta 178-252"
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Protein 22.327
/note "Mature OciF-DDD2"
Misc_difference 273..274
Mide "Positition of deletion, delta 253-326"
                                                                                                                                                                                              Location/Qualifiers
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R99940 standard; Protein; 326 AA.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                     "Signal peptide"
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osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DDD2 in which amino acids 25-326 of the mature OCIF protein are deleted. The OCIF protein are deleted. The OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. and is lost after 10 mins at 70 deg.C. corgr is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Claim 53: Page 111-113; 183pp; Japanese.
This sequence represents a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence represents OCIF-DCR4 in which amino acids 123-164 of the
mature OCIF protein are delated. The OCIF of the invention
has a molecular weight by SDS-PAGE of 60 Bunder reducing conditions
and 120 kD under non-reducing conditions. The protein is adsorbed onto
cation-exchangers or heparin and its activity is lowered after 10 mins
at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
deg.C. OCIF is useful in the control of bone resorption and therefore
in the treatment and prevention of disorders of bone resorption, e.g.
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Mutated OCIF, OCIF-DCR4.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 59; Page 115-116; 183pp; Japanese.
This sequence represents a mutated version of the full length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 20; Length 327;
Pred. No. 2.01e+01;
0; Mismatches 0; Indels
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Pred. No. 2.01e+01;
0; Mismatches 0; Indels
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOCO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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/note="Mature OCIF-DCR4"
/note="Positition of deletion, delta 123-164"
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Best Local Similarity 100.0%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 AA;
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2 YHFPK

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for bone resorption control, esp. treatment in the forbest of claim 47; Page 107-109; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR2 in which amino acids 43-84 of the mature OCIF protein are delated. The OCIF ob under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or hepatin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                       Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutated OCIF, OCIF-DCR3. OSteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding osteoclastogenesis inhibitory factor protein - useful
                                                                                                                                                                                                                                                                                                                         Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 20; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Mature OCIF-DCR3"
Misc_difference 105..106
/note= "Position of deletion, delta 85-122"
                                                                                                                                                                Protein 22..359
/note= "Mature OCIF-DCR2"
Misc_difference 63..64
/note= "Position of deletion, delta 43-84"
                                                                                                                          Location/Qualifiers
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R99937 standard; Protein; 359 AA.
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R99938 standard; Protein; 360 AA.
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Best Local Similarity 100.0%;
Matches 5; Conservative
                                            23-APR-1997 (first entry) Mutated OCIF, OCIF-DCR2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide 1...../note= "Signal peptide" 22..360
                                                                                                                                                     /note= "Signal peptide"
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 AA;
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                              R99937;
23-APR-1997
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NA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim SO, Page 109-111; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR3 in which amino acids 85-122 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto action-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR1 in which amino acids 2-42 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Mutated OCIF, OCIF-DCR1.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoprosis.
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Yasuda H;
                                     Morinaga T
Yasuda H;
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Pred. No. 2.01e+01;
0; Mismatches 0; Indels
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI, 96-402320/40.
N-PSDB; T33168.
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N-PSDB; T33166.
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/note= "Position of deletion, delta 2-42"
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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R99936 standard; Protein; 360 AA.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 AA;
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Score 47; DB 20; Length 360; Pred. No. 2.01e+01;

Query Match Best Local Similarity 100.0%;

DNA encoding osteoclastogenesis inhibitory factor protein - useful

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Mutaked OCIF, OCIF-CBst.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                               22-Apr.1997 (first entry) Mature osteoclastogenesis inhibitory factor. Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 6; Page 62-64; 183pp; Japanese.
This sequence represents the meture osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C., and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Yasuda H;
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 20; Length 380; Pred. No. 2.01e+01; 0; Mismatches 0; Indels
    Indels
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0
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20-FED-1996; JP-054977.
21-JUL-1995; JP-207508.
(SNOW BRAND MILK PROD CO LTD.
GCto M. Higabhlo K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T36685.
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21-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashlo K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI, 96-402320/40.
0; Mismatches
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Best Local Similarity 100.0%;
Matches 5; Conservative
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/note= "Mature OCIF-CBst"
Misc_difference 392
/label= Gla77Leu
WO9626217-A1.
    5; Conservative
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/note= "Signal peptide"
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WO9626217-Al.
29-AUG-1996.
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Matches
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Tor bone resorption control, esp. treatment of osteoporosis

Claim 80; Page 126-128; 183pp; Japanese.

This sequence represents a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence represents OCIF-CBst in which Gln 371 is substituted by
Leu and amino acids 373-380 of the mature OCIF protein are deleted.
These changes are caused by the introduction of a restriction site in
the DNA encoding this protein. The OCIF of the invention has a
molecular weight by SDS-PAGE of 60 Nb under reducing conditions.

and 120 Nb under non-reducing conditions. The protein is adsorbed onto
cation-exchangers or heparin and its activity is lowered after 10 mins
at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 6 deg.C. ocif is useful in the control of bone resorption and therefore
in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1997 (first entry)
Mutated OCIF, OCIF-CL.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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This sequence represents a mutated version of the full length
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                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 20; Length 393;
Pred. No. 2.01e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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20-FEB-1995; JP-05497.
21-UDL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LID.
(SOLOW ) Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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R99942 standard; Protein; 399 AA.
                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide 1..21
/note= "Signal peptide"
Protein 22..399
/note= "Mature OCIF-CL"
                                                                                                                                                                                                                                                                                                                                                393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 yhfpk 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 yhfpk 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T3317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9626217-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 YHFPK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis
                                                                                                                                                                                                                                                                                                                                osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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|||||||| 2 YHFPK 6

Morinaga T;

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Kobayashi
                                            Tsuda E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 100.0%;
Local Similarity 100.0%;
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein 22..401
/note= "Mature OCIF-C195"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Signal peptide"
Goto M, Higashio K, Nakagawa N, Shima N, WPI; 96-402320/40. N-PSDB; T33162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc_difference 195
/label= C195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 yhfpk 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 YHFPK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoporosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 41. Page 103-105; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C23S in which the 23rd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg. C, and is lost after 10 mins at 90 deg. C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                    Mutated OCIF, OCIF-C23S. () OSteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutated OCIF, OCIF-C203.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morinaga T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 20; Length 401
Pred. No. 2.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-1996; JO0374.
20-FEB-1995; JP-084977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                    /F 11
R99935 standard, Protein, 401 AA.
R99935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JT 12
R99932 standard; Protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            Peptide | 1..21 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 
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Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                22-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein 22..401
/note= "Mature OCIF-C20S"
Misc_difference 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-1996.
20-FEB-1996; J00374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 96-402320/40.
N-PSDB; T33165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 yhfpk 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- C20S
WO9626217-A1.
                                                                                                                                                                                                                                                                                                    osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-1996.
                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R99932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
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Wright and osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 3.7 Rage 96-98. I83pp. Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C20S in which the 20th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 Wounder reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto eation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mr. DDA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 29; Page 94-96; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C19S in which the 19th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C. and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AFR-1997 (first entry)
Mutated OCIF, OCIF-C19S.
Osteopolastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morinaga T;
Yasuda H;
                                          Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 20; Length 401; Pred. No. 2.01e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 20; Length 401,
Pred. No. 2.016+01;
'''nma+rhes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09626217-A1.
20-AUG-1996.
20-FEB-1995; JP-054977.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-057508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M, H1gashio K, Kobayashi F, Mochizuki S, Mc Nagawa N, Shima N, Tsuda E, Ueda M, Yano K, Ya NPF: 96-402320/40.
F, Mochizuki S,
Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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401 AA;
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δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 38. Page 100-102, 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C225 in which the 22nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg. C, and is lost after 10 mins at 70 deg. C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                         R99934;
22-ARR-1997 (first entry)
Mutaded OCIF, OCIF-C22S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= C225

W09626217-A1.

20-406-1996.

20-FEB-1996. J00374.

20-FEB-1995. JP-054977.

21-JUL-1995. JP-057508.

(SNOW) SNOW BRAND MILK PROD CO LTD.

GOto M. Higashio K. Kobayashi F. Mochizuki S. Mo

Nakaqawa N. Shima N. Tsuda E. Ueda M. Yano K. Ya

NPI: 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                  T 114
R99934 standard; Protein; 401 AA.
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/note= "Mature OCIF-C228"
Misc_difference 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Signal peptide"
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                         355 yhfpk 359
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/note= "s
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This sequence represents the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Full length osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Score 47; DB 20; Length 401;

Best Local Similarity 100.0%; Pred. No. 2.01e+01;

Matches 5; Conservative 0; Mismatches 0; Indels
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Pred. No. 2.01e+01;
0; Mismatches 0; Indels
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29-AUG-1996.
20-FEB-1995; JP-054977.
20-FEB-1995; JP-207508.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOTO M, Higgshio K, Kobayashi F, Mochizuki S, Mor Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yas WPI; 96-402320.440.
20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-205408.
(SNOW BRAND MILK PROD CO LTD.
GCto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33163.
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/note= "Mature OCIF, claim 6"
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Best Local Similarity 100.0%;
Matches 5; Conservative
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/note= "Signal peptide"
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= zinc-finger
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                                                                                                                                                                                                                                                                                                                                                                                           peregrin protein"
720 yqfpk 724
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2 YHFPK 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA fragment contg. gene for detecting resistance -
to kanamycin and gentamycin from Streptococcus plasmid, and new
expression prod. for making hybridisation probes
Claim 6; Page 27 and Fig 3; 34pp; French.
SO in n81668 codes for a protein imparting resistance to kanamycin and
gentamycin. The DNA is useful for making hybridisation probes to detect
kanamycin and gentamycin resistance in clinically-isolated cell cultures.
Sequence 505 AA,
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                                                                                                                                                                                              12-DEC-1990 (first entry) Sequence encoded by part of AAC(6')-APH(2'') (6'-acetlytransferase-2''-phosphotransferase) gene in the plasmid pIP800 of Streptococcus faecalis JH 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Human tumour suppressor protein HTS-1 (R90766) is produced by procaryotic or eucaryotic host cells transformed or transfected by a vector including an isolated HTS-1 coNA (T12473). Expression of HTS-1 is associated with tumour suppression. The purified HTS-1 protein can be used to raise antibodies for use in HTS-1 detection. Sequence 1137 AA.
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Tumour suppressor protein HTS-1.
Tumour suppressor protein; HTS-1; cancer; therapy; prognosis.
                                                                                                                                                                                                                                                                                                                     gentamycin resistant; Staphylococcus; antibiotic resistant.
Streptococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                               Streptococcal plasmid pGB3012; kanamycin resistant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 15;
Pred. No. 8.43e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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17-JUL-1992; 916762.
17-JUL-1992; US-916762.
05-JAN-1995; US-369043.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
HOWLEY PM, LICHY JH;
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                                                                                                                                                   P81265 standard; protein; 505 AA.
P81265;
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25-JUL-1986. 010829.
25-JUL-1986. FR-010829.
(CNRS) Cent Nat Rech Sci (INSP).
COULYALIN P.
WPI: 88-079435/12.
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ilarity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 91.5%;
Local Similarity 80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ey PM, Lichy JH;
96-116319/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; n81668.
                355 yhfpk 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 yhypk 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
US5491064-A.
                                                          2 YHFPK 6
                                                                                                                                                                                                                                                                                                                                                                FR2601965-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 YHFPK 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis and treatment of leukaemias, partic, acute
lymphoblastic or nonlymphoblastic leukaemia
[Jaim 53; Page 134-135; 207pp; English.
Monoclonal antibodies which bind to at least part of the chimeric
ALL-L/AR-17 protein (R66459) or to part of the AR-17 protein (see
R66460 and R66461) are claimed. The antibodies are useful for
diagnosing acute lymphoblastic and non-lymphoblastic leukaemia.
                                                              AF-17 protein, N-terminal region with similarity to peregrin. Acute lymphoblastic leukaemia, chromosomal translocation; abnormality, detection; chimeric ALL-1/AF-17 protein; ALL-1 fused gene on chromosome 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R23005;
29-OCT-1992 (first entry)
Protein transcribed from the mba sequence of plasmid pKDSC50.
Virulent; Salmonella choleraesuis; mouse bacteremia; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canaani E, Croce C;
WPI; 95-006818/01.
New acute lymphocytic leukaemia gene prods. - used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                               /note= "region of 90% identity to anonymous human cDNA sequence (Genbank Acc.No.To6113)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 12; Pred. No. 1.47e+02;
                                                                                                                                                                                                                     /note= "cysteine-rich region with similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           W0942050.
24-NOV-1994.
22-APR-1994; U04496.
14-MAY-1993; US-065443.
(UYJE-) UNIV JEFFERSON THOMAS.
R66461 standard; Protein; 188 AA.
R66461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .T 20
R23005 standard; Protein; 255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-1990; 194069.
24-JUL-1990: JP-194069.
(KIBU-) KIBUN KK.
(KITA.) KITASAPO RES INST.
WPI; 92-137918/17.
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Best Local Similarity 80.0%;
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Three other proteins may also be transcribed from the Salmonella
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The receptor binds to TNF, and in particular, TNF-beta.

The receptor may be used for screening for antigonists and agonists of the receptor may be used for screening for antigonists may be used to inhibit the growth of tumours, to stimulate cellular differentiation, to mediate the immune response and anti-viral response, to regulate growth and provide resistance to certain infections. The antagonists may be used therapeutically, to treat autoimmune diseases, inflammation, septic shock, to inhibit graft-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JÄN-1997 (first entry).
Daundrubicin 14-hydroxylase.
daundrubicin 14-hydroxylase.
                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1997 (first entry)
Muman tumour necrosis factor receptor.
Tumour necrosis factor TNF: receptor: TNF-beta; ligand; tumour;
differentiation; immune response; autoimmune disease; inflammation;
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0
"mba" fragment, which is capable of causing mouse bacteremia. See also R23004-7.
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Pred. No. 1.47e+02;
0; Mismatches 0; Indels
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20-FEB-1996; B00692.
27-FEB-1995; US-396218.
(PHAA, ) PHARMACIA SPA.
Breme U, Colombo AL, Hutchinson CR, Otten S, Scotti C;
                                                                                                                              Score 40; DB 4; Lengtn 20, Pred. No. 1.47e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      versus-host reactions, and to prevent apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      septilc shock; graft-versus-host; apoptosis.
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WO9627014-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 21
R99337 standard; Protein; 390 AA.
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15-MAR-1995; WO-U03216.
15-MAR-1995; AC-002587.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative
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WO9628546-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann RD, G1
WPI; 96-433821/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 AA;
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                                                                                                                                                                                                                                                                                    yhfp 138
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                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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claim 4; Page 15:18; 31pp; English.

The present sequence is that of the daunorubicin 14-hydroxylase, isolated from Streptomyces peucetius strain 2005. The enzyme converts daunorubicin to doxorubicin, an anthracycline used widely as an antitumour agent. A vector contg. the drxA gene (733617) could be used to transform a suitable host cell which produces daunorubicin, in order to enhance bioconversion of daunorubicin to doxorubicin. Bioconversion can be carried out either by using directly the free or immobilised transformed cells or by isolating the enzyme, which can be used in the free form or immobilised to resins, glass, cellulose or similar substances by ionic or covalent bonds, or graffed to fibres permeable to the substrate or insolubilised by cross-linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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The present sequence is the Exophiala spinifera (ATCC 74269) The present sequence is the Exophiala spinifera (ATCC 74269) The present sequence is the Exophiala spinifera (ATCC 74269) The present sequence is the Exophiala spinifera (ATCC 74269) The present sequence is the Exophiala spinifera (ATCC 74269) The present sequence or temperature of the microcorganisms, capable of pants and genetically engineered microcorganisms, capable of expressing the esterase. The microcorganisms can be used as a problem of the processed grain of the harvested grain, or in the processed grain) prior to its use as an animal feed.
Solari INVENTI A, Inventi AS;
WPI; 96-412780/41.
N-PSDB; T33617.
New DNA encoding daunorubicin 14-hydroxylase - useful for converting
daunorubicin to the antitumour agent doxorubicin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exophiala spinifera fumonisin esterase. Fumonisin: esterase; transgento plant; recombinant microorganism; expression; probiotic; feed inoculant; degradation; detoxification; maize seed; grain; annal feed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 19; Length 422;
Pred. No. 1.47e+02;
0; Mismatches 0; Indels
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R14402 standard; Protein; 934 AA.
R14402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R91277 standard; Protein; 527 AA.
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07-UTN-1995; US-484815.
(PION-) PIONEER HI-BRED INT INC.
DUVICK J. ROOM TA.
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Best Local Similarity 100.0%;
Matches 4; Conservative
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Best Local Similarity 80.0%;
Matches 4; Conservative
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11-AUG-1995; U10284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 96-151378/15
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including exons from two separate receptors, having improved growth performance in serum-free medium bisclosure; Fig 3: 57pp; English.

The amino acid sequence is that of the soluble insulin-like growth factor (IGF) receptor. It is used here as part of a fusion protein produced by a hybrid DNA insert comprising a DNA sequence encoding part of the extracellular domain of the IR and a sequence coding for part of the ECD of an insulin like growth factor (IGF). Cells contg. this insert have better growth characteristics in both serum-contg. and partic. serum-free media. This makes them useful for expressing polypeptides (e.g. human blood clotting factors; issue plasminogen activator; human protein C), encoded by a third DNA sequence. The polypeptides of an now be purified more easily and produced in better yield. See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New hybrid cellular receptor - has 2 sequences encoding extracellular domain of receptors having different ligand binding extracellular domain of receptors having different ligand binding provided by 37pp; English.

Proposition of the sequence was deduced from a cDNA sequence prepd. from mRNA isolated from human term placenta by PCR amplification. The full sequence was assembled from four subcloned fragments and was found to be identical to that published by Ullrich et al. (The EMBO Ournal 5(120), 1986, pp 2503-2512). The DNA can be ligated to DNA encoding a sol. insulin receptor (see 014813) to prepare hybrid proteins. The new receptors are useful for screening for ligands of control collising the ligand binding site. They are also useful for establishing the 3-D structure of the ligand binding site and control of the sequence or functional equivalents.
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                                                                                                                                                                                                                            Mammalian cells contg. hybrid DNA for extracellular receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 3; Length 934; Pred. No. 1.47e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 3; Length 934;
Pred. No. 1.47e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kjeldsen T, Andersen AS, Wiberg F, Moller N, Rasmussen J;
WPI; 91-353773/48.
N-PSDB; Q14814.
                                                                                    14-NOV-1991.
30-APR-1991; DK0116.
30-APR-1990; DK-001064.
(NOVO ) NOVO NORDISK A/S.
Wiberg FC, Olsen F, Boel E, Kjeldsen TB, Moller NPH
WPI; 91-353774/48.
14-FEB-1992 (first entry)
Soluble Insulin-like Growth Factor receptor.
Extracellular receptor; IGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R15048 standard; Protein; 934 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RI5048;
14-FEB-1992 (first entry)
Soluble human IGF-I receptor.
Insulin-like growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.1%;
larity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-1990; DK-001855.
(NOVO ) NOVO NORDISK A/S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-1991.
30-APR-1991; DK0115.
30-APR-1990; DK-001063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     934 AA;
                                                                                                                                                                                    WPI; 91-353/79
N-PSDB;Q14380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
WO9117252-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 YHFPK 6
                                                                                  14-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  also R14403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Matches
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Gaps

.; 0

85.1%; 80.0%; Conservative

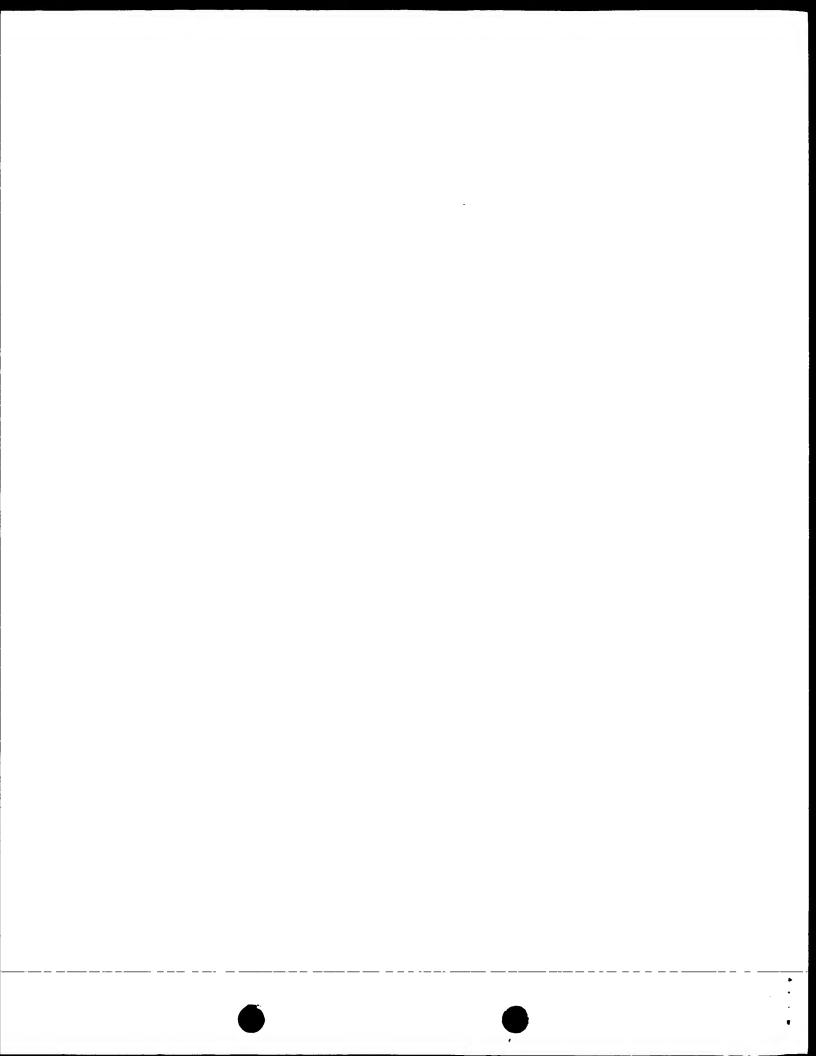
Local Similarity

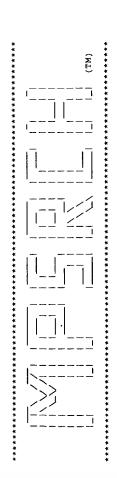
Best Loc Matches

Query Match

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Mammalian cells contg, hybrid DNA for extracellular receptor including exons from two separate receptors, having improved strowth performance in serum-free medium Disclosure; Fig 4: 57pp; English.

The amino acid sequence is that encoded by a hybrid DNA insert comprising a DNA sequence encoding part of the extracellular domain of the IR and a sequence coding for part of the ECD of an insulin like growth factor (IGF). Cells contg, this insert have better growth characteristics in both serum-contg, and partic. serum-free media. This makes them useful contexing polypeptides (e.g. human blood clotting factors; tissue plasminogen activator; human protein C), encoded by a third DNA sequence. The polypeptides can now be purified more easily and procedured in better yield. See also R14402.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                            14-FEB-1992 (first entry)
Extracellular domain of hybrid insulin/IGF-I receptor.
Extracellular receptor; IGF; fusion protein.
                                                                                                                                                                                                                                      30-APR-1991; DK0116.
30-APR-1990; DK-001064.
(NOVO ) NOVO NORDISK A/S.
Wiberg FC, Olsen F, Boel E, Kjeldsen TB, Moller NPH.
WPI; 91-353774/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: Wed Dec 3 10:06:32 1997 Job time: 12 secs.
                                                                                                           R14403 standard; Protein; 948 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
75 yrfpk 79
                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q14380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 yrfpk 77
                   |:|||
2 YHFPK 6
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2 YHFPK 6
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:43:12 1997; MasPar time 5.65 Seconds 30.699 Million cell updates/sec Run on:

>US-08-915-004-1 (1-6) from US08915004.pep 47 ular output not generated. tle:

1 XYHFPK 6 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

91006 segs, 28888923 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

l:annl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 20.106; Variance 27.499; scale 0.731

Statistics:

SUMMARIES

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	No	0+6	8e+00	0+	88e+0	88e+0	0 +	88e+0:	88e+0	41e+0	41e+01	41e+01	41e+0	41e+0	0	0+1	0+6	1e+0	1e+0	1e+0.	0+6	0 +	
	Pred.	96e+00	96e	88e+0	886	886	88e+0	88	886	41e	.41€	41e	.416	.416	.41e+0	.41e+0	.41e+0	.416	416	416	.41e+01	.41e+01	
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CHINAMACC	QI	A56101	B56101	A26048	S26353	A41793	168600	I54331	S32613	S58182	S58186	S58184	A44275	S42791	S42793	A47092		S52763	A49013	S23353	S23352	860932	
	DB	14	14	σ	σ	14	13	13	11	16	16	16	4	12	12	σ	16	11	13	12	12	12	
	Length	103	562	479	479	803	803	865	1014	109	109	109	109	228	264	336	349	349	645	700	705	1511	
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æ	Query Match	100.0	100.	91.5	91	91	91	91.5	91	89.4	88	8	8	8	83	8	83	89	89	8	8	83	
	Score	47	47	43	43	43	43	43	43	42	42	42	42	42	42	42	42	42	42	42	42	42	
	Sult No.	-	7	m	4	S	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	

#formal_mame Mus musculus #common_name house mouse 03-0ct-1995 #sequence_revision 03-0ct-1995 #text_change 03-0ct-1995 #sequence_revision 03-0ct-1995 #text_change 03-0ct-1995 #sequence_revision 03-0ct-1995 #text_change 1856101
Rehn, M.; Pihlajaniemi, T.
J. Biol. Chem. (1995) 270:4705-4711

ACCESSIONS REFERENCE #authors #journal

ORGANISM

DATE

41 87.2 238 9 139731 hydrogenase small ch 6.70e+01 24 40 85.1 252 10 832053 hypothetical protein 6.70e+01 25 40 85.1 209 16. \$62589 hypothetical protein 1.01e+02 26 40 85.1 27 10 842653 56 Forbit 1.01e+02 27 40 85.1 283 11 \$46770 56 Forbit 1.01e+02 28 40 85.1 327 10 842653 56 Forbetical protein 1.01e+02 29 40 85.1 348 4 MFNZS matrix protein - Sen 1.01e+02 31 40 85.1 351 8 B49906 Forbit 1.01e+02 32 40 85.1 351 8 B49906 hypothetical protein 1.01e+02 33 40 85.1 361 9 155054 rfbB protein - Sen 1.01e+02 34 40 85.1 361 9 155054 rfbB protein - Shige 1.01e+02 35 40 85.1 361 9 155054 rfbB protein - Shige 1.01e+02 36 40 85.1 361 9 155059 major early-transcri 1.01e+02 37 40 85.1 361 9 155059 major early-transcri 1.01e+02 38 40 85.1 1 449 8 A45709 major early-transcri 1.01e+02 39 40 85.1 624 10 A55220 penicillin-binding p 1.01e+02 40 85.1 1021 14 A57112 mourdeat protein SON 1.01e+02 41 40 85.1 1289 1 RMXRR3 mRNA guanylytransfe 1.01e+02 42 44 40 85.1 1371 5 A33837 insulin-like growth 1.01e+02	ALIGNMENTS II 1 A56101 #type fragment Collagen alpha 1(XVIII) chain precursor short form - mouse (fragment) (fragment) #formal_name Mus musculus #common_name house mouse 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995 A56101 A56101 A56101 A56101 A56101 Identification of three N-terminal ends of type XVIII collagen chains and tissue-specific differences in the expression of the corresponding transcripts. The longest form contains a novel motif homologous to rat and brosophila frizzled proteins. Drosophila frizzled proteins. Bresidues 1-103 ##label REH ##residues COLUBAL #RECOSS-references GB:U11636 COLUBAL ARY #Inength 103 #checksum 5841 #RY 100.0%; Score 47; DB 14; Length 103; stt. Local Similarity 100.0%; Pred. NO. 4.96e+00; LINE 7 WATCH 2 YHFPK 6	NLT 2 8Y B56101 #type fragment NL collagen alpha 1(XVIII) chain precursor long form - mouse
	RESULT TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors #journal #title ##rec ##rec GENETICS SUMMARY OUGTY MAT BEST LOCE MATCHES OUGTY MAT BEST LOCE MATCHES Db 74 1	RESULT ENTRY TITLE

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Gaps

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##cross-references EMBL:M18086
##note the authors translated the codon GAT for residue 374 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wada, K.; Yokotani, N.; Hunter, C.; Doi, K.; Wenthold, R.J.; Shimasaki, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dipeptidyl aminopeptidase-like protein (EC 3.4.14..) short form, DPPX-S - bovine form, beame Bos prinigenius taurus #common_name cattle 04.Nar-1993 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:197-201
#title Differential expression of two distinct forms of mRNA encoding members of a dipeptidyl aminopeptidase family.
#cross-references MUID:92108018
#accession A41793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #binding_site carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168600 #type complete diperity aminopeptidase like protein - human dipeptida Homo sapiens #common_name man 06-5ep-1996 #sequence_revision 06-Sep-1996 #text_change
                                                                                                                                            #molecular-weight 56855 #checksum 5383
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#length 803 #molecular-weight 90459 #checksum 9315
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91.5%; Score 43; DB 14; Length 803;
Best Local Similarity 80.0%; Pred. No. 2.88e+01;
Matches 4; Conservative 1; Mismatches 0; Indels
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##molecule_type mRNA
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                                                                                                                                                                                                     Score 43; DB 9; Length 479;
Pred. No. 2.88e+01;
1; Mismatches 0; Indels
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                                                                                                                                                                                                     Query Match 91.5%;
Best Local Similarity 80.0%;
Matches 4; Conservative
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##residues 1-80:
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                                                                                                       KEYWORDS
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J. Gen. Microbiol. (1987) 13:3039-3052
The aacA-aphD gentamicin and kanamycin resistance determinant
of In4001 from Staphylococcus aureus: expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $26353  #type complete aminoqlycoside resistance protein aacA-aphD - Staphylococcus aureus transposon Th4001  #formal_name Staphylococcus aureus  #formal_name Staphylococcus aureus  03-May-1994  #sequence_revision 20-Feb-1995  #text_change
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Identification of three N-terminal ends of type XVIII collagen chains and tissue-specific differences in the expression of the corresponding transcripts. The longest form contains a novel motif homologous to rat and Droscophila frizzled proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors | Ferretti, J.J.; Gilmore, K.S.; Courvalin, P. |
#journal J. Bacteriol. (1986) 167.631-638 |
#title Nucleotide sequence analysis of the gene specifying the bifunctional 6'-aminoglycoside acetyltransferase |
2"-aminoglycoside phosphotransferase enzyme in Streptococcus faecalis and identification and cloning of gene regions specifying the two activities. |
#cross_references MUID:86277923 |
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aminoglycoside acetyltransferase - Enterococcus faecalis
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05_Oct-1988 #sequence_revision 05-Oct-1988 #text_change
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##molecule_type mRNA
##residues 1-562 ##label REH
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##cross-references EMBL:M90540
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#journal Mol. Cell. Biol. (1992) 12:2673-2680

#title SRN, a yeast gene involved in RNA processing, is identical to HEX2/REC1, a negative regulator in glucose repression.

#cross-references MUID:92269840
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HEX2 protein - yeast (Saccharomyces cerevisiae)
Protein D3402: protein P2F240: protein YD9813.06c; protein YD8028c; SRN1 protein #formal_name Saccharomyces cerevisiae
#formal_name Saccharomyces cerevisiae
30-Sep-1993  #sequence_revision 30-Sep-1993  #text_change
                                                                                                                                                                                                                                                                                             Yokotani, N.; Doi, K.; Wenthold, R.J.; Wada, K. Hum. Mol. Genet. (1993) 2:1037-1039 Non-conservation of a catalytic residue in a dipeptidyl aminopeptidase IV-related protein encoded by a gene on
                                                                                                                                                         dipeptidyl aminopeptidase like protein - human #formal_name Homo sapiens #common_name man 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1996
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submitted to the EMBL Data Library, January 1994
S50935
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##residues 1-865 ##label RES
##cross-references GB:M96859; NID:g306705; CDS_PID:g306706
XY #length 865 #molecular-weight 97587 #checksum
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Pred. No. 2.88e+01;
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##molecule_type DNA
""----:Anas 962-1014 ##label TU2
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##cross-references EMBL:247814
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##residues 1-1014 ##label TU1
##cross-references EMBL:M90540
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                Similarity 80.0%;
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##residues 1-375,'EE',378-533,'K',535-656,'H',658-888,'T',890-987,
##residues 1-375,'EE',378-533,'K',535-656,'H',658-888,'T',890-987,
##cross-references EMBL:M33703

"FERENCE 563416
#authors Eide, L.G.; Sander, C.; Prydz, H.
#submission submitted to the EMBL Data Library, February 1996
#description Sequencing and analysis of a 35.4 kb region on the left arm of chromosome IV for Saccharomyces cerevisiae reveal 23
pen reading frames.
#accession 563438
##residues 775-1014 ##label EID
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#authors Niederacher, D.; Entian, K.D.
#journal Eur. J. Biochem. (1991) 200:311-319
#title Characterization of Hex2 protein, a negative regulatory element necessary for glucose repression in yeast.
#cross-references MUID:91364678
#accession S17254
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submitted to the Protein Sequence Database, July 1996
S67841
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#length 1014 #molecular-weight 112615 #checksum
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91.5%; Score 43; DB 11; Length 1014;
Best Local Similarity 80.0%; Pred. No. 2.88e+01;
Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     S27374
Niederacher, D.; Entian, K.D.
S2mhitted to the EMBL Data Library, April 1990
S27374
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##residues 775-1014 ##label PRY
##cross-references EMBL:274324
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NCE S67822
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nonstructural protein, 12.8K - porcine hemagglutinating
encephalomyelitis virus (strain w972)
#formal_name porcine hemagglutinating encephalomyelitis virus
13.Jan-1996 #sequence_revision 13.Jan-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nonstructural protein, 12.8K - porcine hemagglutinating encephalomyelitis virus (strain MP9)
encephalomyelitis virus (strain MP9)
encephalomyelitis virus 13.Jan-1996 #sequence_revision 13.Jan-1996 #text_change
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nonstructural protein NS2 - human coronavirus (strain OC43)
#formal_name human coronavirus
17-Feb-1994 #text_change
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1-109 ##label VIE
##cdoss-references EMBL:X89863
** # elength 109 #molecular-weight 12818 #checksum 4120
                                                ##cdoss-references EMBL:X89861
Y #holecular-weight 12818 #checksum 4120
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##redsidues 1-109 ##label VIE
##crposs-references RMBL:X89862
*# elength 109 #molecular-weight 12773 #checksum 4821
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Pred. No. 4.41e+01;
1; Mismatches 0; Indels
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1; Mismatches 0; Indels
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Best Local Similarity 80.0%;
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#domain fork head DNA-binding domain homology #label FHD #length 228 #molecular-weight 25752 #checksum 8289
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                         Mounir, S.; Talbot, P.J.
Virology (1993) 192:355-360
Human coronavirus Oc43 RNA 4 lacks two open reading frames located downstream of the S gene of bovine coronavirus. A44275
                                                                                                                                842791 #type complete
PES-1B protein - Caenorhabditis elegans
#formal_name Caenorhabditis elegans
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
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06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
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##residues 1-264 ##label_HO2
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##residues 1-264 ##label E
##cross-references EMBL: Z28375
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A47092 #type complete
replication protein repA - Enterococcus faecalis plasmid pADI
#formal lname Enterococcus faecalis
26-May-1994 #sequence_revision 26-May-1994 #text_change
26-May-1994
A47092
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A47092
Identification, characterization, and nucleotide sequence of a region of Enterococcus faecalis pheromone-responsive
plasmid pADI capable of autonomous replication.
                                     #domain fork head DNA-binding domain homology #label FHD #length 264 #molecular-weight 29480 #checksum 3098
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plasmid
#length 336 #molecular-weight 39031 #checksum 4594
#superfamily fork head DNA-binding domain homology
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##residues 1-33
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Search completed: Tue Dec 2 14:43:23 1997 Job time : 11 secs.

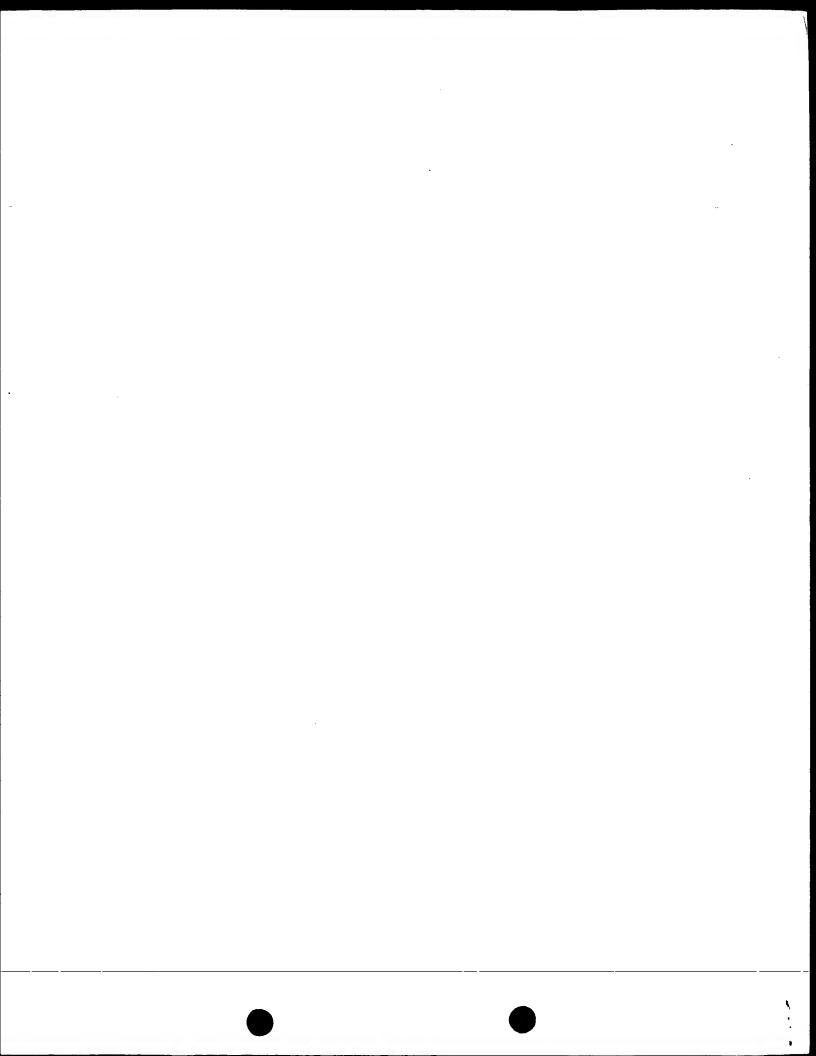
18 yqfpk 22 |:||| 2 YHFPK 6

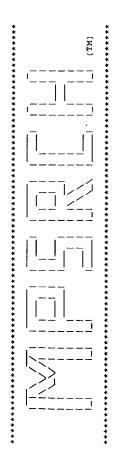
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:42:45 1997; MasPar time 3.82 Seconds 33.352 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-1 (1-6) from US08915004.pep 47 tle:

1 XYHFPK 6 Description: Perfect Score: Sequence:

59021 seqs, 21210388 residues PAM 150 Gap 15 Searched:

Scoring table:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 20.932; Variance 22.971; scale 0.911 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Length	DB	ID	Description	Pred. No.
1	47	100.0	1315	. ~	CA1H_MOUSE	COLLAGEN ALPHA 1(XVII	9.76e-01
7	43	91.5	479	Н	AACA_STAAU	6'-AMINOGLYCOSIDE N-A	7.96e+00
m	43	91.5	859	æ	DPP6_RAT	DIPEPTIDYL PEPTIDASE	7.96e+00
4	43	91.5	863	m	DPP6_BOVIN		7.96e+00
S	43	91.5	865	m	DPP6_HUMAN	DIPEPTIDYL PEPTIDASE	7.96e+00
o	43	91.5	1014	4	HEX2_YEAST	HEX2 PROTEIN (SRN1 PR	7.96e+00
7	42	89.4	109	10	VNS2_CVHOC	NONSTRUCTURAL PROTEIN	1.32e+01
8	42	4.68	349	11	YJY9_YEAST	HYPOTHETICAL 40.3 KD	1.32e + 01
σ	41	87.2	252	11	YCR2_BACTK	HYPOTHETICAL 29.1 KD	2.16e+01
10	40	85.1	101	σ	TRAL_SALTY	TRAL PROTEIN.	3.51e+01
11	40	85.1	209	11	YAL4_SCHPO	HYPOTHETICAL 23.8 KD	3.51e+01
12	40	85.1	255	10	VRP1_SALEN	28.1 KD VIRULENCE PRO	3.51e+01
13	40	85.1	255	10	VRP1_SALDU	28.1 KD VIRULENCE PRO	3.51e+01
14	40	85.1	255	10	VRP1_SALCH	28.1 KD VIRULENCE PRO	3.51e+01
15	40	85.1	262	7	COX3_ANOGA	CYTOCHROME C OXIDASE	3.51e+01
16	40	85.1	283	11	YHWO_YEAST	HYPOTHETICAL 32.0 KD	3.51e+01
17	40	85.1	291	11	YLF4_CAEEL	HYPOTHETICAL 34.1 KD	3.51e+01
18	40	85.1	323	σ	SYK3_HAEIN	HYPOTHETICAL LYSYL-TR	3.51e+01
19	40	85.1	325	σ	SYK3_ECOLI	HYPOTHETICAL LYSYL-TR	3.51e+01
20	40	85.1	327	7	ODPB_ACHLA	PYRUVATE DEHYDROGENAS	3.51e+01
21	40	85.1	337	11	YJEQ_ECOLI	HYPOTHETICAL 37.7 KD	3.51e+01
22	40	85.1	348	10	VMAT_SEND5	MATRIX PROTEIN.	3.51e+01

3.51e+011 3.51e+011 3.51e+011 3.51e+011 3.51e+011 3.51e+011 3.51e+011 3.51e+011 3.51e+011 3.51e+011 3.51e+011 3.51e+011
MATRIX PROTEIN. MATRIX PROTEIN. MATRIX PROTEIN. HYPOTHETICAL 42.2 KD HYPOTHETICAL 40.3 KD HYPOTHETICAL 41.7 KD HYPOTHETICAL 44.5 KD HYPOTHETICAL 63.8 KD CLUSTERIN PRECURSOR (EARLY 53 KD PROTEIN (EARLY 53 KD PROTEIN (EARLY 53 KD PROTEIN (EARLY 54.5 KD HYPOTHETICAL 63.8 KD USYLL-TRNA SYNTHETASE SERING-THREONINE PROT HYPOTHETICAL 63.8 KD GLUCAN ENDO-1,3-BETA- SERINE/THREONINE PROT PUTALIYE GLUCOSAMINE- COUTACTIN PRECURSOR (ZINC FINGER PROTEIN S INSULN-LIKE GROWTH F
VMAT_SENDF VMAT_SENDP VMAT_SENDP VMAT_SENDS VC54_HAEIN VD6B_SCHPO VJFR_ECOLI AVPLECOLI AVPLECOLI AVPLECOLI AVPLECOLI AVPLECOLI AVPLEMAN VMS3_YEAST VMS5_YEAST VMS5_YEAST VMS5_YEAST VMS5_YEAST VMS5_YEAST VMS1_HOWAN MES3_NOVAN MES3_NO
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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ALIGNMENTS

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Gaps

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Score 43; DB 1; Length 479; Pred. No. 7.96e+00; 1; Mismatches 0; Indels

SIMILARITY). 479 AA; 56855 MW; A8193B91 CRC32;

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Query Match 91.5%;
Best Local Similarity 80.0%;
Matches 4; Conservative
                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYL-COA BINDING SITE (BY SIMILARITY).
TO OTHERS APHS AND A VPH.
AMINOGLYCOSIDE SUBSTRATES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACA_STAAU STANDARD; PRT; 479 AA.
P14507;
01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-OGT-1994 (REL. 30, LAST ANNOTATION UPDATE)
6'-AMINOGLYCOSIDE N-ACETYLTRANSFERASE (EC 2.3.1.-) (AAC(6')) / 2''-AMINOGLYCOSIDE PHOSPHOTRANSFERASE (EC 2.7.1.-) (AAC(6')).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 86277923.
FERRETTI J.J., GILMORE K.S., COURVALIN P.;
FERRETTI J.J., GILMORE K.S., COURVALIN P.;
J. BACTERIOL. 167.631-638(1986).
-!- FÜNCTION: RESISTANCE TO GENTAMICIN, TOBRAMYCIN, AND KANAMYCIN. RESISTANCE IS DUE TO THE ACC ACTIVITY, SPECIFIED BY THE FIRST 170 AA, AND THE GENTAMICIN RESISTANCE IS DUE TO THE APH ACTIVITY ENCODED BY THE C-TERMINAL REGION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLTRANSFERASE FROM S.LAVENDULAE. THE C-TERMINAL REGION IS HOMOLOGOUS TO OTHERS APHS, AND TO A VIOMYCIN PHOSPHOTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACA JAPHD.
STAPHYLOCOCCUS AUREUS, AND ENTEROCOCCUS FAECALIS (STREPTOCOCCUS
                                                                                                                                                                                                                                                      TRIPLE-HELICAL REGION 9 (COL9).
NONHELICAL REGION 10 (NC10).
TRIPLE-HELICAL REGION 10 (COL10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                               CELL ATTACHMENT SITE (POTENTIAL)
MW; FAE26C53 CRC32;
                                                                                                       NONHELICAL REGION 6 (NC6).
TRIPLE-HELICAL REGION 6 (COL6).
NONHELICAL REGION 7 (NC7).
                                                               NONHELICAL REGION 5 (NC5).
TRIPLE-HELICAL REGION 5 (COL5).
                                                                                                                                                                       (COL7).
                                                                                                                                                                                                              TRIPLE-HELICAL REGION 8 (COL8).
NONHELICAL REGION 9 (NC9).
    TRIPLE-HELICAL REGION 3 (COL3).
                                         REGION 4 (COL4).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1315;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 2; Length 1315
Pred. No. 9.76e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      NONHELICAL REGION 11 (NC11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M13771; G153586; --
EMBL; M18086; G152948; --
EMBL; M26048; A256048; --
PIR; S26333; 256533; ANTIBIOTIC RESISTANCE; TRANSFERASE; KINASE; ATP-BINDING; ACTITRANSFERASE; TRANSPOSABLE ELEMENT.
                                                                                                                                                                                           (NC8)
                                                                                                                                                                       TRIPLE-HELICAL REGION 7
NONHELICAL REGION 8 (NC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROUCH D.A., BYRNE M.E., KONG Y.C., SKURRAY R.A.;
J. GEN. MICROBIOL. 133:3039-3052(1987).
                      NONHELICAL REGION
TRIPLE-HELICAL REC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROKARYOTA; FIRMICUTES; COCCI; MICROCOCCACEAE
                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SPECIES-S.AUREUS; TRANSPOSON-IN4001;
MEDLINE; 88187650.
                                                                                                                                                                                                                                                                                                                                                                                                       134263
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                               892 89
1315 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yhfpk 78
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                                                                                                                                                                                                                                                                                                                                                                                   SITE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.,
PROC. NATL. ACAD. SCI. U. S.A. 89:197-201(1992).

1 PROC. NATL. ACAD. SCI. U. S.A. 89:197-201(1992).

2 PUNCTION: MAY BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
FUNCTION: HAS NO DIPEPTION. AMINOPEPTIOASE ACTIVITY. THE LACK OF
ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE
FOR THE SERINE RESIDUE IN THE PROPOSED CATALITY. THE LACK OF

2 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROPERIN (PROBABLE).

3 SPECIFICITY: DPPX-S IS EXPRESSED IN BRAIN AND SOME
PRINPHARAL TISSUES NATURED ALONGY EXCLUSIVELY IN BRAIN.

4 CONTRAST DPPX-L IS EXPRESSED ALMOST EXCLUSIVELY IN BRAIN.

5 ALTERNATIVE PRODUCTS: TWO.DISTINCT FORMS (DPPX-L AND -S) SHARE AN

5 IDENTICAL TRANSMEMBRANE DOMAIN AND A LONG C-TERMINAL EXTRACELLULAR

5 DOMAIN, BUT HAVE LONG AND SHORT N-TERMINAL CYTOPLASMIC DOMAINS.

5 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE

5 EMBL; M76428; 6408714; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
SIGNAL-ANCHOR; ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                    DPP6_RAT
DPP6_RAT
DPP6_RAT
DPP6_RAT
DP46101;
01-NOY-1995 (REL. 32, CREATED)
01-NOY-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-REB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DIPEPTIDXL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDXL AMINOPEPTIDASE-RELATED PROTEIN) (DIPEPTIDXL PROTEIN), (DIPEPTIDASE-VI) (DIPEPTIDXL PROTEIN), 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGPQAQAVAPRERGGAGGRPRFQYQARSDCDEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 7.96e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKEPSASGKSVQQQDQ (IN DPPX-S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
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Best Local Similarity 80.0%;
Matches 4; Conservative
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86 yhypk 90
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CARBOHYD
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RC TISSUE-BRAIN;

A MEDLINE; 92108018.

RA WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.;

RA WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.;

RL PROC. NATL. ACAD. SCI. U.S.A. 98:197-201(1992).

CC -!- FUNCTION. HAX BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN

CC ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPATATE RESIDUE

PORTHE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRAD.

-!- SUBGELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).

-!- SIBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).

-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN. DPDX-L.

IS EXPRESSED EXCLUSIVELY IN THE BRAIN WHEREAS DPPX-S IS FOUND IN CC -!- ALTERNATIVE SPLICITY: A SHORT FORM (DPPX-S) AND A LONG FORM (DPPX-L).

CC -!- SIMILANTY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLICE SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).

CC -!- SIMILANTY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC.

CC -- SIMILANTY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC.

CC -- SIMILANTY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC.

CC -- SIMILANTY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC.

CC -- SIMILANTY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC.

CC -- SIMILANTY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC.

CC -- SIMILANTY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC.

CC -- SIMILANDEN SIMILANDEN SIMILANDEN SIGNAL-ANCHOR; ALTERNATIVE SPLICING.

FT TRANSMEM SIGNAL-ANCHOR; ALTERNATIVE SPLICING.

FT TRANSMEM S9 4 114 SIGNAL-ANCHOR.
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PLGAQAPAAAPREKGGGGGGGGRPRFQYQARSDCDDED ->
MTTAKEPNASGKSVQQQEQ (IN DPPX-S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
          DPP6_BOVIN STANDARD; PRT; 863 AA.
P42659;
01.NOV-1995 (REL. 32, CREATED)
01.NOV-1995 (REL. 33, LAST SEQUENCE UPDATE)
01.FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DIPPEPTIDXL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-RELATED PROTEIN) (DIPPEPTIDASE VI) (DPPX-L/DPPX-S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DIPEPRIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-
RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
                                                                                                                                                                        BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 3; Length 863;
Pred. No. 7.96e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8DA40472 CRC32;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     863 AA; 96556 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.5%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                            EUTHERIA; ARTIODACTYLA.
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171
171
402
469
469
533
533
564
811
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Best Local Similarity
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DPP6_HUMAN
P42658;
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CARBOHYD
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CARBOHYD
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VARSPLIC
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REPGPRAQAAPRERGGGGGAGGRPRGYQGRSDGDEED
-> MTTAREPSASGSVQQDEQE (IN DPPX-S).
514C21E2 CRC32;
                       MEDLINE; 93372805.

YOKOTANI N. DOI K., WENTHOLD R.J., WADA K.;

HUM. MOL. GENET. 2:1037-1039(193).

-!-FINCTION: MAY BE INVOLUED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
FUNCTION: MAY BE DIVED TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE
FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.

-!- SUBCELLUAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBBLE).

-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN.

-!- TISSUE SPECIFICITY: ASPRESSED PREDOMINANTLY IN BRAIN.

-!- TISSUE SPECIFICITY: BERODICES A SHORT FORM (DPPX-S) AND A LONG FORM (DPPX-L).

-!- SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).

-!- SHUMLARTIY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM: 126141; -
HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
SIGNAL-ANCHOR; ALTERNAIIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HEXZ PROTEIN (SRN1 PROTEIN).
HEXZ OK SRN1 OR REGIOR SPP43 OR YDR028C OR YD9813.06C.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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STRAIN-S288C / AB972;
BOWMAN S., BARRELL B., RAJANDREAM M.A.;
SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 3; Le
Pred. No. 7.96e+00;
1; Mismatches 0
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POTENTIAL.
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MEDILINE; 91364678
NIEDERACHER D., ENTIAN K.-D.;
EUR. J. BIOCHEM. 200:311-319(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROLYL OLIGOPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 775-1014 FROM N.A. EIDE L.G., SANDER C., PRYDZ H.;
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M96859; G306706;
EMBL; M96860; G306708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319
404
471
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1173
319
404
471
535
813
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HEX2_YEAST
Q00816;
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TRANSMEM
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CARBOHYD
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CARBOHYD
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CARBOHYD
VARSPLIC
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NAME OF THE OF T
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RESULT 10
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ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
DK -> EE (IN REF. 1).
N -> K (IN REF. 1).
D -> H (IN REF. 1).
S -> T (IN REF. 1).
S -> T (IN REF. 1).
LOCALIZATION SIGNAL (POTENTIAL).
LOCALIZATION SIGNAL (POTENTIAL).
LOCALIZATION SIGNAL (POTENTIAL).
LOCALIZATION SIGNAL (POTENTIAL).
LOCALIZATION SIGNAL SIGNA
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12:1085-1090(1996).
PROCESSING AND NEGATIVE REGULATION OF CLUCOSE REPRESSION. REGULATES THE LEVEL OF TWO ANTIGENS, P43 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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01-FÉB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FÉB-1994 (REL. 28, LAST ANNOTATION UPDATE)
NONSTRUCTURAL PROTEIN NSZ NONSTRUCTURAL 12.9 KD PROTEIN).
HUMAN CORONAVIRUS (STRAIN OC43).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; CORONAVIRIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 4; Length 1014;
Pred. No. 7.96e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 10; Length 109; Pred. No. 1.32e+01; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IN REF. 1).
1014 AA; 112615 MW; 65BA11F7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 93297129.
MOUNIR S., TALBOT P.J.;
MOUNIR S., TALBOT P.J.;
EMBL; M99576; G329568. -.
PIR; A44275; A44275.
MOUNTRUCTURAL PROTEIN.
SEQUÈNCE 109 AA; 12935 MW; C47B6812 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 109 AA.
                                                                                                                                                                           SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 89.4%;
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                         EMBL, M33703, G171666; --
EMBL, M90540; G172699; --
EMBL, Z47814; G642300; --
EMBL, X55966; E225541; --
PIR; S17254; S17254.
PIR; S32613; S32613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LISTA: SC00434; HEX2.
SGD; L0001609; REG1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 yhypk 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YHFPK 6
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2 YHFPK 6
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YCR2_BACTK STANDARD; PRT; 252 AA.
1921733.
01-MAY-1991 (REL. 18, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
14YPOTHETICAL 29-11 KD PROTEIN IN CRYB1 S'REGION (ORF2).
BACILLUS THURINGTENSIS (SUBSP. KURSTAKI).
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 2.16e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 11; Length 349; Pred. No. 1.32e+01; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 X 15 AA TANDEM REPEATS.
                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
DE HAAN M., SAITS P.H.M., CRIVELL L.A.;
DE HASI M., SAITS P.H.M., CRIVELL L.A.;
DE HASI W.S. SAITS P.H.M., CRIVELL L.A.;
EMBL; X85972; G758285; --
EMBL; X87611; G854594; --
EMBL; Z49519; G1015655; --
HYPOTHETICAL PROTEIN.
SEQUENCE 349 AA; 40259 MW; C38D06E2 CRC32;
                                                                                                                    HANI J., STUMPF G., DOMDEY H.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2B6BECAB CRC32;
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12 (INCOMPLETE).
13 (INCOMPLETE).
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MEDLINE; 89123178.
MIDLINE; 89123178.
J. BACTERIOL. 171:965-974(1989).
EMBL, MA3723; G1124821;
PIR, B12053; B32053.
HYPOTHETICAL PROTEIN; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29110 MW;
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 80.0%;
Matches 4; Conservative
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                                                                                SEQUENCE FROM N.A.
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YJR019C OR J1456
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                                                                                                   STRAIN-DH484;
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SEQUENCE FROM N.A.
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2 YHFP 5
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VRP1_SALDU
P24418;
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                     SALMONELLA TYPHIMURIUM.
PLASAND PED2008.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
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MCLEAN J., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: TO YEAST SPT10.
EMBL; 267999; G106720;
-HYPOTHETICAL PROTEIN.
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                                                                                                                                                                                                                                                                                                                  Score 40; DB 11; Length 209;
Pred. No. 3.51e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.1%; Score 40; DB 9; Length 101; larity 80.0%; Pred. No. 3.51e+01; Conservative 1; Mismatches 0; Indels
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNORATION UPDATE)
HYPOTHETICAL 23.8 KD PROTEIN C21E11.04 IN CHROMOSOME I.
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SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
BUKARYOTA: FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 AA; 23809 MW; DA251012 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLASMID; CONJUGATION; OUTER MEMBRANE.
SEQUENCE 101 AA; 12037 MW; 941A2072 CRC32;
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                  01-0CT-1989 (REL. 12, CREATED)
01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Best Local Similarity 100.0%;
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Matches 4; Conserv
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                                                                                                                   TRAL PROTEIN.
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Q09927;
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANABROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
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MEDLINE; 91251759.
MEDLINE; 91251759.
MCDLINE; O., FIERER J., HARWOOD J., GUINEY D.;
MOL. MICROBIOL. 5:307-316(1991).
-!- FUNCTION: NOT KNOWN. THIS PROTEIN IS INVOLVED IN THE VIRULENCE
OF SALMONELLAS.
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                                                                                                                                                                                                                            Length 255;
                                                                                                                                                                                                            Score 40; DB 10; Length 2>>
Pred. No. 3.51e+01;
"...matches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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01-A0G-1990 (REL. 15, CREATED)
01-ANG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
28.1 KD VIRGLENCE PROTEIN (PROTEIN M3, IN MBA REGION).
PLASMIONELLA CHOLERAE-SUIS (SALMONELLA ENTERICA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 10; Le
Pred. No. 3.51e+01;
0; Mismatches 0;
                                                                                                                       EMBL, X56727; G47838; -.
PIR; S15214; S15214.
PLASMID; VIRULENCE.
SEQUENCE 255 AA; 28156 MW; 2455A4CB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-1992 (REL. 21, CREATED)
01-WAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-WAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
28.1 KD VIRULENCE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  255 AA
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                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SALMONELLA DUBLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-RF-1;
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                                                                                                                                                                                                                                0; Gaps
                            NUCLETIC ACIDS RES. 18:2181-2181(1990).
-!- FUNCTION: NOT KNOWN. THIS PROTEIN IS INVOLVED IN THE VIRULENCE OF SALMONELLAS.
-!- SIMILARITY: TO SIMILAR PROTEIN IN OTHER SALMONELLA VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-G3;

BEARD [C.B., HAMM D.M., COLLINS F.H.;

INSECT MOL. BIOL. 2:103-104(1993).

-!-FÜNCTION: SUBGNIT I, II, AND III FORM THE FUNCTIONAL CORE OF THE BRIZHE COMPLEX.

-!-CATALYTIC ACTIVITY. 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.

EMBL; LOG934; G3030962, -

OXIDOREDUCTAASE; MITOCHONDRION; TRANSMEMBRANE.

SEQUENCE 262 AA; 30132 MW; 73CE1E48 CRC32;
                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 3.51e+01;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tery Match 85.1%; Score 40; DB 2; Length 262; st Local Similarity 80.0%; Pred. No. 3.51e+01; ltches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANOPHELES GAMBIAE (AFRICAN MALARIA MOSQUITO).
MITOCHONDRION.
EUKARĶOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
                                                                                             PLASMIDS.
EMBL, X52035; 646897; -.
PLR, S09497; S09497.
SEQUENCE 255 AA; 28184 MW; ECBB81FC CRC32;
                                                                                                                                                                                                                                                                                                                                                          262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: Tue Dec 2 14:42:53 1997 Job time : \mid 8 \text{ secs.}
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
MEDLINE; 90245675.
MATSUI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 yhfsk 230
                                                                                                                                                                                                                                                        . 135 yhfp 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | : |
2 YHFPK 6
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Dec 3 10:06:49 1997; MasPar time 5.21 Seconds 33.068 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-2 (1-14) from US08915004.pep 78 1 XQHSXQEQIFQLXK 14 Description: Perfect Score: Itle:

Scoring table:

Sequence:

PAM 150 Gap 15

101610 seqs, 12294212 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq28
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21

Mean 16.442; Variance 48.941; scale 0.336 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.43e-02	2.43e - 02	2.43e - 02	2.43e - 02	2.43e-02	2.43e-02	2.43e-02	2.43e - 02	2.43e - 02	2.43e-02	2.43e-02	2.43e-02	1.19e+02							
Description	Osteoclastogenesis in	Mutated OCIF, OCIF-CD	Mutated OCIF, OCIF-CS	Mutated OCIF, OCIF-DD	Mutated OCIF, OCIF-CC	Mutated OCIF, OCIF-DC	Mutated OCIF, OCIF-DC	Mutated OCIF, OCIF-DC	Mutated OCIF, OCIF-DC	Mature osteoclastogen	Human tumour necrosis	Mutated OCIF, OCIF-CB	Mutated OCIF, OCIF-CL	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C1	Full length osteoclas	Prostate-specific mem
Ωi	R99922	R99944	R99949	R99941	R99943	R99939	R99937	R99938	R99936	R99924	R99357	R99948	R99942	R99934	R99932	R99935	R99933	R99931	R99925	W02241
Length DB	14 20	272 20	321 20	327 20	351 20	359 20	359 20	360 20	7	380 20	390 20	7	7	401 20	401 20	~	~	~	401 20	22 18
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	59.0
Score	78	78	78	7.8	7.8	78	78	78	78	78	7.8	78	78	78	78	78	78	78	78	46
sult No.	-	7	ю	4	Ŋ	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20

1.19e+02 1.19e+02 1.19e+02 1.19e+02 1.19e+02 1.19e+02 1.19e+02 1.19e+02 1.19e+02 1.15e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.52e+02 1.54e+02 1.5
Prostate-specific mem Human auxillary cytoc Human auxillary cytoc Human cytochrome P450 Human cytochrome P450 Secretory alkaline ph Germ cell alkaline ph Human germ cell alkaline ph Human germ specific mem Prostate-specific mem Chicken TRADD intracell E75B exon B1 polypept Chicken TEF-1B. JMI-229 cell line t-P RPTP-beta amino acid Human RPTP-beta. JMI-229 cell line t-P RPTP-beta amino acid Human RPTP-beta. Bovine interferon alp Sequence of bovine le Bovine interferon alp Bat-PA(L). V-PA_beta. Bat-PA(L).
R55102 R72368 R72368 R93174 R81466 R93175 R50100 R95234 R50527 R70523 R3528 R13528 R78275 R78
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44944 44944 44944 44944 4494 4493 4493
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ALIGNMENTS

Score 78; DB 20; Length 14; Pred. No. 2.43e-02; 0; Mismatches 0; Indels Query Match 100.0%; Best Local Similarity 100.0%; Matches 13; Conservative

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Gaps

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2 qhsxqeqtfqlxk 14 g

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243 ghssqeqtfqllk 255
        N-PSDB; T33179.
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                                                                                                                                                             23-APR-1997 (first entry)
Mutated OCIF, OCIF-CDD2.
Ostebclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutated OCIF, OCIF-CSph.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Yasuda H;
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 78; DB 20; Length 272;
Pred. No. 2.43e-02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-1996.
20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-UEL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSpB; Ţ33174.
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20-FEB-1995; JP-05497.
21-UTL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(GOLO M. Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; ]96-402320/40.
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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R99944 standard; Protein; 272 AA.
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Best Local Similarity 84.68;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        Protein 22..272 // note = "Mature OCIF-CDD2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein 22.321
/note= "Mature OCIF-CSph"
                                                                                                                                                                                                                                                                                                                                    Peptide 1..21
/note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 qhssqeqtfqllk 255
  OHSXQEQTFOLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QHSXQEQTFQLXK 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                             W09626217-A1.
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                                                                                                                                                                                                                                                     osteoporosis.
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                                                                                    RESULT
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The according osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 8; page 128-129; 188pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CSph in which amino acids 298-380 of the mature COIF protein are replaced by Ser-Leu-Asp. These changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducting conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.c or 30 mins at 56 deg.c, and is lost after 10 mins at 90 deg.c. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DDD2 in which amino acids 253-326 of the mature OCIF protein are deleted. The OCIF of the invention on and 120 Kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C ociF is useful in the control of bone resorption and therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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23-APR-1997 (first entry)
Mutated OCIF, OCIF-DDD2.
Osteoclastcogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 78; DB 20; Length 321; Best Local Similarity 84.6%; Pred. No. 2.43e-02; Matches 11; Conservative 0; Mismatches 2; Indels
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Wiemarches 2; Indels
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Pred. No. 2.43e-02;
0; Mismatches 2; Indels
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Robayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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Misc_difference 273..274
/note= "Positition of deletion, delta 253-326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Best Local Similarity 84.6%;
Matches 11; Conservative
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/note= "Mature OCIF-DDD2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 qhssqeqtfqllk 255
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N-PSDB; T3317
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RESULT

ID DOT DOT ET FT PD PD

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Yasuda H;

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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 47, Page 107-109, 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR2 in which amino acids 43-84 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 470 deg.C. ocif is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                           osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR4 in which amino acids 123-164 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1997 (first entry)
Mutated OCIF, OCIF-DCR2.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                               DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 53; Page 111-113; 183pp; Japanese.
This sequence represents a mutated version of the full length
                                                                                                                                                                                                                                                                                                                                                                                              , DB 20; Leuy-.
. 2.43e-02;
. 2. Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-1996.
20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSDB; T33167.
F, Mochizuki S,
Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc_difference 63..64
/note= "Position of deletion, delta 43-84"
                                                                                                                                                                                                                                                                                                                                                                                                               Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  л 7
R99937 standard; Protein; 359 AA.
  Kobayashi
                     Tsuda E,
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
84.6%;
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6%;
Matches 11; Conservative
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/note= "Mature OCIF-DCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..21
"Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 qhssqeqtfqllk 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 OHSXQEQTFQLXK 14
Goto M, Higashio K,
Nakagawa N, Shima N,
WPI; 96-402320/40.
N-PSDB; T33169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc_difference 63
                                                                                                                                                                                                                                                                                                                                                                        359 AA;
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                                                                                                                                                                                                                                                                                                                                                       osteoporosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis (laim 65; Page 119-121; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CC in which amino acids 331-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutated OCIF, OCIF-DCR4.
                                                                                                                                                                                 Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morinaga T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 78; DB 20; Length 351;
Pred. No. 2.43e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-1996; JO0374.
20-FEB-1995; JP-05497.
21-071-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc_difference 143 .144
/note= "Positition of deletion, delta 123-164"
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-057508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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R99939 standard; Protein; 359 AA.
                                                                               T 5
R99943 standard; Protein; 351 AA.
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84.6%;
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                                                                                                                                        23-APR-1997 (first entry)
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/note= "Mature OCIF-DCR4"
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                                                                                                                                                                                                                                                                Peptide 1.21
/note= "Signal peptide"
Protein 22.351
/note= "Mature OCIF-CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 qhssqeqtfqllk 255
                                                                                                                                                                Mutated OCIF, OCIF-CC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 QHSXQEQTFQLXK 14
                   2 OHSXOEOTFOLXK 14
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  351 AA;
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WO9626217-Al.
                                                                                                                                                                                                        osteoporosis.
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Gaps

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Gaps

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Morinaga T; Yasuda H;

Peptide

'note=

R99939;

RESULT

Matches

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                                                                                                                                                                                                                                                                                                                                            DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 50. Page 109-111; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR3 in which amino acids 85-122 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto action-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. Or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                              23-AFR-1997 (first entry)
Mutațed OCIF, OCIF-DCR3.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutated OCIF, OCIF-DCRI.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                     Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 78; DB 20; Length 360;
Pred. No. 2.43e-02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                      20-FEB-1996; JO0374.
20-FEB-1996; JP-054977.
21-JUL-1995; JP-207508.
5NOW BRAND MILK PROD CO LTD.
GCtO | M. Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSPB; T33168.
                                                                                                                                                                                                         Misc_difference 105..106
/note= "Position of deletion, delta 85-122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Signal peptide"
Protein 22.360
/note= "Marure OCIF-DCRI"
Misclafiference 22.23
/note= "Position of deletion, delta 2-42"
                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                              .T |8
R99938 standard; Protein; 360 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R99936 standard; Protein; 360 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 100.0%;
Local Similarity 84.6%;
les 11; Conservative
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                                                                                                                                                                                   Protéin // Anture OCIF-DCR3" / Anture OCIF-DCR3"
                                                                                                                                                                   1..21
"Signal peptide"
        201 qhssqeqtfqllk 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 qhssqeqtfqllk 217
                              2 OHSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QHSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 AA;
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29-AUG-1996.
                                                                                                                                 osteoporosis.
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for bone resorption control, esp. treatment of osteoporosis.
Claim 44; Page 105-107; 183pp; Japanese.
This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents oCIF-DCRI in which amino acids 2-42 of the areure oCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto action-exchangers or hepzin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Mature osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In the encoding osteoclastogenesis inhibitory factor, protein - useful for bone resorption control, esp. treatment of osteoporosis claim 6; Page 62-64; 183pp; Japanese.

This sequence represents the mature osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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29-ACG-1996.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio R, Kobayashi F, Mochizuki S, Morinaga T;
Wakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
WPI; 96-402320/40.
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Yasuda H;
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Pred. No. 2.43e-02;
0; Mismatches 2; Indels
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Pred. No. 2.43e-02;
0; Mismatches 2; Indels
20-FEB-1996; J00374.
R 20-FEB-1995; JP-054977.
R 21-JUL-1995; JP-207508.
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
PA (SNOW ) F. M. Higashio K, Kobayashi F, Mochizuki S, Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R99924 standard; Protein; 380 AA.
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Homo sapiens
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for treating e.g. tumours, infection, auto:immune disease, graft rejection, cytotoxicity or inflammation
Claim 14: Fig 1: 59pp: English.
The receptor binds to TNF, and in particular, TNF-beta.
The receptor may be used for screening for antagonists and agonists of the receptor and for ligands for the receptor. Such agonists be used to inhibit the growth of tumours, to stimulate cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                 Human tumour necrosis factor receptor.
Tumour necrosis facor; TNF; receptor; TNF-beta; ligand; tumour;
differentiation; immune response; autoimmune disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentiation, to mediate the immune response and anti-viral response, to regulate growth and provide resistance to certain infections. The antagonists may be used therapeutically, to treat autoimmune diseases, inflammation, septic shock, to inhibit graft-versus-host reactions, and to prevent apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human tumour necrosis factor receptor - used to develop prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 390;
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20-FEB-1996; J003/4.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(SNOW ) Higashio K, Kobayashi F, Mochizuki S, Higashio K, Kobayashi F, Wochizuki S, Mochizuki S, Mochizuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78; DB 20; Dred. No. 2.43e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                             septic shock; graft-versus-host; apoptosis.
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R99948 standard; Protein; 393 AA.
                           R99357 standard; Protein; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 100.0%;
Local Similarity 84.6%;
                                                                                     05-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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/note= "Mature OCIF-CBst"
Misc_difference 392
/label= Gln371Leu
                                                                                                                                                                                                                                                                                                                                                                                   19-SEP-1996.
15-MAR-1995; U03216.
15-MAR-1995; WO-U03216.
29-MAR-1995; ZA-002587.
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                                                                                                                                                                                                                                                                                                                            /label= sig_peptide WO9628546-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fleischmann RD, Gr
WPI; 96-433821/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T35475
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                                                                                                                                                                                                                                         Homo sapiens.
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                                                       R99357;
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RESULT
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                                                                                            osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CBst in which Gln 371 is substituted by leu and amino acids 373-380 of the mature OCIF protein are deleted. These changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C. and Mins at 56 deg. C, and is lost after 10 mins at 90 deg. C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutated OCIF, OCIF-CL.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                         This sequence represents a mutated version of the full length
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Pred. No. 2.43e-02;
...matrhes 2; Indels
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21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashi F, Mochizuki S,
Nakagawa M, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
Claim 80; Page 126-128; 183pp; Japanese
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Matches 11; Conservative
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/note= "Signal peptide"
Protein 22..399
/note= "Mature OCIF-CL"
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20-FEB-1996; J00374.
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243 qhssqeqtfqllk 255
         N-PSDB; T33162
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Matches
                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                  DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 38; Page 100-102; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C22S in which the 23nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation exchanges or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the protein and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                            22-Apr-1997 (first entry)
Mutated OCIF, OCIF-C22S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                          Morinaga T;
Yasuda H;
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 78; DB 20; Length 401;
Pred. No. 2.43e-02;
0; Mismatches 2; Indels
                                                                                                                                                                             29-4021996.
20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLD M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33164.
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29-AUG-1996.
20-FEB-1995; JD-054977.
21-UUL-1995; JP-054977.
21-UUL-1995; JP-207508.
GSNOW ) SNOW BRAND MILK PROD CO LTD.
GOCOM , Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
                                                                                       Location/Qualifiers
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       R99934 standard; Protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7. 15
R99932 standard; Protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
84.6%;
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//note= "Signal peptide"
Protein 22.401
//note= "Mature OCIF-C205"
Misc_difference 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.6%;
Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1997 (first entry)
                                                                                                                        Protein 22..401 /note= "Mature OCIF-C225"
                                                                                                 Peptide 1..21
/note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutated OCIF, OCIF-C20S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 qhssqeqtfqllk 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QHSXQEQTFQLXK 14
                                                                                                                                    /note= "Mature OCIF"
Misc_difference 277
                                                                                                                                                         /label= C22S
W09626217-A1.
                                                                  osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                       osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= C20S
                                                                           Synthetic.
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 3.7 Page 96-98; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C20S in which the 20th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 41, Page 103-105, 183pp; Japanses.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C23S in which the 23rd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 78; DB 20; Length 401;
Pred. No. 2.43e-02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78; DB 20; Length 401;
Pred. No. 2.43e-02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-1996; JO0374.
20-FEB-1996; JP-054977.
21-JUL-1995; JP-054977.
SNOW BRAND MILK PROD CO LTD.
GCto M, Higashio K, Kobayashi F, Mochizuki S,
Nakaqawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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R99935 standard; Protein; 401 AA.
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Best Local Similarity 84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein 22..401
/note= "Mature OCIF-C23S"
Misc_difference 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 qhssqeqtfqllk 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QHSXQEQTFOLXK 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 AA;
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- useful

Morinaga T;

F, Mochizuki S, Ueda M, Yano K,

Yasuda H;

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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents offreci9s in which the 19th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                     DNA encoding osteoclastogenesis inhibitory factor protein for bone resorption control, esp. treatment of osteoporosis Claim 29; Page 94-96; 183pp; Japanese.
  21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
                              Goto M, Higashio K, Kobayashi F, Makagawa N, Shima N, Tsuda E, Ued WPI; 96-40232/40.
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                        243 qhssqeqtfqllk 255
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                                                                                                                                                                                                                                                                        osteoporosis
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                                                                                  22-APR-1997 (first entry)
Mutated OCIF, OCIF-C21S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutated OCIF, OCIF-C19S. OSTEOCIE: OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 35; Page 98-100; 183pp; Japanese.
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Yasuda H;
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Pred. No. 2.43e-02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                           20-FEB-1996; JO0374.
21-FEB-1996; JP-054977.
21-JUL-1995; JP-207508.
(SNOW BRAND MILK PROD CO LTD.
GGto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; Ţ33163.
                                                                                                                                                                      Location/Qualifiers
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                                                      JT 17
R99933 standard; Protein; 401 AA.
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Local Similarity 84.6%;
hes 11; Conservative
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                                                                                                                                                                                                       Protein 22..401 /note= "Mature OCIF-C215"
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Misc_difference 195
                                                                                                                                                                                 Peptide 1..21
/note= "Signal peptide"
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2 QHSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QHSXQEQTFQLXK 14
                                                                                                                                                                                                                                        Misc_difference 277
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20-FEB-1996; J00374.
20-FEB-1995; JP-0549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 AA;
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W09626217-A1.
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                                                                                                                                                                                                                                                                                 29-AUG-1996
                                                                                                                                                        Synthetic.
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Gaps

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Length 401;

Score 78; DB 20; Length 401, Pred. No. 2.43e-02;

401 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Disclosure; Page 64-66; 183pp; Japanese.

This sequence represents the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                            22-APR-1997 (first entry)
Full length osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
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Pred. No. 2.43e-02;
"'..matches 2; Indels
                                                                                                                                                                                                                                                                                                                                                    29-700-1996
20-FEB-1996; J00374.
20-FEB-1995; JP-05497.
21-U1-1995; JP-07508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T36685.
                                                                                                                                                                                                 Location/Qualifiers
R99925 standard; Protein; 401 AA.
                                                                                                                                                                                                                                                                         Protein 22..401
/note= "Mature OCIF, claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                     Peptide 1..21
/note= "Signal peptide"
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                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                          DNA encoding alternatively spliced prostate-specific membrane antigen - useful to develop prods. for detecting haematogenous micromenestic tumour cells, or prostate cancer progression Example 1; Page 49; 284pp; English.

Tryptic peptides (W02237-45) were obtd. from the human prostate-specific membrane (PSM) antigen (see also W0224) and used to design primers (T36795-808) utilised in the isolation of a CDNA clone (T36785) coding for PSM; primers 1.L (T36801.04) are based on amino acids 14-19 of peptide 2734 6 (W02241). The isolated CDNA and PSM protein are useful in developing methods for the diagnosis and treatment of prostate cancer and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate-specific membrane antigen peptide fragment.
Prostate-specific membrane antigen; PSM; prostate cancer;
transmembrane glycoprotein; imaging; targeting; tumour detection;
antibody detection; sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fair WR, Heston WDW, Israeli RS; WPI: 94-167129/20. Prostate-specific membrane antigen and DNA encoding it - is useful for detecting haematogenous micro-metastatic tumour cells and for identifying ligands which bind to PSM Ag Example; Page 46; 196pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                            Prostate-specific membrane antigen peptide 2T34 6.
Prostate-specific membrane antigen; PSM; prostate cancer;
metaștasis; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 59.0%; Score 46; DB 18; Length 22; Best Local Similarity 75.0%; Pred. No. 1.19e+02; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                           (SLOK ) SLOAN KETTERING INST CANCER RES.
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                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                /note= "unidentified amino acid"
Misc_difference 5
/note= "unidentified amino acid"
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R551ģ2 standard; Peptide; 22 AA.
                                                          W02241 standard; Peptide; 22 AA.
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/note= "unidentified residue"
Misc_difference 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                  (first entry)
                                                                                                                                                                                                                29-AŭG-1996.
23-FEB-1996: U02424.
24-FEB-1995: US-394152.
02-JÜN-1995: US-460315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MÀY-1994.
05-NOV-1993; U10624.
05-NOV-1992; US-973337.
OHSXQEQTFQLXK 14
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                                                                                                                                                         Misc_difference 4
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                                                                                                                                   Homo|sapiens.
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                                                                                 05-Nov-1996
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                                                                                                                                                                                                                                                                                        Fair
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Avaluation of safety of a chemical cpd. - using recombinant yeast
expressing human cytochrome p450 and a yeast NADPH-P450 reductase
Examples; Page 49-51; 124ppp. English.

Examples; Page 49-51; 124ppp. English.

The amino acid sequence of the human auxillary cytochrome P450 species

2A6. The cDNA was amplified by PCR using the primers Q87751-4. The
product was coloned into the yeast expression of the cytochrome P450 alone
or p2A6R for co-expression with the yeast NADPH-P450 reductase.

The vectors are used in a method for evaluating the safety of a chemical
compound by reacting the chemical compound with recombinantly produced
human cytochrome P450 molecular species 1A2 (Q87714), 2C9 (Q87718-3), and yeast NADPH-P450 reductase, either as a fused protein or
in cellextracts, and analysing the resulting metabolite to assess the
safety of the chemical compound. The method is useful for determining
whether the chemical compound, or its metabolite, will be converted into
sequence 494 AA.
The inventors attempted to sequence the PSM Ag by modified Edman degradation. Peptides (R55098-107) that gave clear dominant peaks on HPLC from the digested PSM Ag sample were used. Some of the residues were unidentified, and others were present at very low levels and identified with lower confidence. Some of these peptides were used to design primers to carry out PCR to identify cDNA clones were used to design primers to carry out PCR to identify cDNA clones canceding the PSM Ag. R55102 was used to design primers Q65527-30.

A clone, IN-20 was identified as a partial PSM sequence. The full PSM Ag sequence is shown in R55097 and is encoded by Q65520). The PSM coding sequence is useful for suppressing or modulating the metastatic ability of prostate tumour cells to grow, or for eliminating them. The PCR is useful to identify or purify ligands of the Ag. It is also an attractive target for Ab-directed imaging and targeting of prostatic tumour deposits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human auxillary cytochrome P450 species 2A6 protein.

Human cytochrome P450; amplification; PCR; primer; expression vector; yeast NADPH-P450 reductase; safety; fusion protein; metabolite; carcinogen; mutagen; liver metabolism.

Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 10; Length 22;
Pred. No. 1.19e+02;
0; Mismatches 2; Indels
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Pred. No. 1.19e+02;
3; Mismatches 1;
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20-JUL-1994; 111298.
20-JUL-1993; JP-201120.
21-JUL-1993; JP-208246.
30-JUL-1993; JP-208279.
(HAYA/) HAYASHI K.
(SUMO) SUMITOMO CHEM CO LID.
HAYASHI K, RANGKO H, KOMAI K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 55.6%;
Matches 5; Conservative
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N-PSDB; T28387
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J08027195-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For a variant of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase Examples; Page 53-55, 124pp; English.

Examples; Page 53-55, 124pp; English.

The amino acid sequence of the human auxillary cytochrome P450 species 2A6 variant 1. This variant contains a variation at residue 476. And to Lys, caused by a variation at base 1427. G to A in the DNA sequence. The CDNA was amplified by PCR using the primers (87751-4. The product was cloned into the yeast expression vectors pAAHSN or pAHRR to produce the vectors p2A6 variant 1 for the expression of the cytochrome P450 alone or p2A6R variant 1 for the expression with the yeast NADPH-P450 reductase. The vectors are used in a method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly produced human cytochrome P450 molecular species 1A2 (087714), 2C9 (087715), 2E1 (087716), or 3A4 (087718), or their auxillary species and variants of callextracts, and analysing the resulting metabolite to assess the safety of the chemical compound, or its metabolite, will be converted into a carcinogenic or mutagenic form through metabolism in the liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-007-1996 (first entry)
Human cytochrome P450 molecular species 2A6 variant #1 protein.
Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
liver; yeast; expression vector; NADPH-P450 reductase; AbH gene promoter;
evaluation; safety; fusion protein; metabolite; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                               14.NOV-1995 (first entry)
Human auxillary cytochrone P450 species 2A6 variant 1 protein.
Human cytochrome P450; amplification; PCR; primer; expression vector;
yeast NADPH-P450 reductase; safety; fusion protein; metabolite;
carcinogen; mutagen; liver metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko H, Komai K, Nakatsuka I, Sakaki T;
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               .r 23
R72368 standard; Protein; 494 AA.
R72368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R93174 standard; Protein; 494 AA.
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20-JUL-1993, JP-201120.
30-JUL-1993, JP-208279.
17-JUN-1994, JP-136053.
(SUMO ) SHMITOMO CHEM CO LID.
WPI; 96-182311/19.
                                                                                                                                                                                                                                                          Misc_difference 476
/note= "Arg to Lys variation"
EP-644267-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUMO ) SUMITOMO CHEM CO LID. Hayashi K, Kaneko H, Komai I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.0%;
Similarity 55.6%;
5; Conservative
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20-JUL-1993; JP-201120.
21-JUL-1993; JP-180246.
30-JUL-1993; JP-208279.
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Best Local Similarity
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J08056695-A.
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               RESULT
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Nursub; 12000.

Novel method for the evaluation of the safety of a cpd. - using a human cytochrome P450 and yeast NaDPH reductase to determine whether the manalyte cpd. is detoxified or metabolised to a carcinogen Example 1; Page 33-35; 74pp; Japanese.

Comparison of the amino acid sequence of the human cytochrome P450 molecular species 2A6 variant #1 protein. The corresp. gene was amplified from a comman liver derived cDNA library as 2 fragments of 0.6 and 0.9 kb using primers 126941-44. The prod. was cloned into the yeast expression vector pAHRR to generate plasmid p2A6 for prodn. of the cytochrome only or into the vector pAHRR to generate the plasmid p2A6 for prodn. of the cytochrome only or into the vector pAHRR to generate the plasmid p2A6 for prodn. of the cytochrome only or into the vector pAHRR to generate the plasmid p2A6 for prodn. of the cytochrome only or into the vector pAHRR to generate the plasmid p2A6 for prodn. of the cytochrome only or into the vectors are used in a method for evaluating the safety of a cpd. by reacting the test cpd. with recombinantly produced human cytochrome P450 compared protein or as a cell (128381), 2E1 (128382), 3A4 (128383) or their variants (128384-98) together with yeast NaDPH-P450 reductase carbitant metabolite. The cpd. is considered safe" if it is not detoxified or is metabolised to a carcinogenic or "unsafe" if it is not detoxified or is metabolised to a carcinogenic or "unsafe" if it is not detoxified or is
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Human derived cytochrome, P4502A6.
Human derived cytochrome, P4502A6; commercial cDNA library; yeast;
transfection; recombinant production; expression vector; mammal;
immunisation; sensitisation; antibody; determination; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody recognising human derived cytochrome P4502A6 - allows specific detection of cytochrome P450 species in humans S Example 1.9 Pages 11-13; 13pp; Japenese.

The present sequence is the human derived cytochrome (HDC) P4502A6, which was obtd. from a commercial cDNA library. Yeast C were transfected with an expression vector confg. the HDC cDNA, cultured and then discupted to qive a microsomal fraction. The HDC was purified from the fraction, and used to immunise and ansensitise a mammal. Blood was drawn from the mammal, and an anti-HDC antibody isolated The antibody obtd. recognises HDC P4502A6, partic. at a serum dilution rate of 1:10000, and is substantially without cross reaction to other HDC P450 spp..
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R81466;
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13-JUL-1994; 161550.
13-JUL-1994; JP-161550.
(SUMO) SUMITOMO CHEM CO LTD.
WPI; 96-136336/14.
N-PSDB; 117409.
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55.68;
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Best Local Similarity 55.6%;
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The R93175 standard; Protein; 494 AA.

AC R93175.

The Coff-1996 (first entry)

The Hunah cytochrome P450 molecular species 2A6 variant #2 protein.

The Coff-1996 (first entry)

We would alon; safety; fusion protein; metabolite; detoxification; primer; yeast, expression vector; NDDH-1450 reductase; ADH gene promoter; we wouldarion; safety; fusion protein; metabolite; detoxification; promoter; arrivogenic.

Shown (saplens.)

Pho 15-MAR-1994

The 1994; JP-1208279.

PR 20-JUJ-1993; JP-2208279.

PR 20-JUJ-1993; JP-2208279.

PR 17-JUM-1994; JP-130829.

Novel method for the evaluation of the safety of a cpd. - using a method for the evaluation of the safety of a carcinogen of the main of a confidence of the method is detoxified or methodised to a carcinogen of the main of sequence of the methodised to a carcinogen of primers (1993; JP-208279).

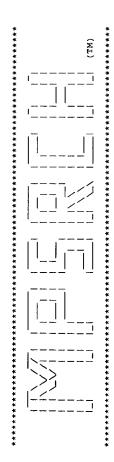
Novel method for the evaluation of the safety of a cpd. - using a hunar cytochrome P450 and yeast NADPH reductase to determine whether the analyte cpd is detoxified or methodised to a carcinogen of primers (1994) and the safety of a cpd. with the crown and the same of the safety of a cpd. by the analyte cpd is detoxified or methodised to a carcinogen of primers (2004) summer (2004) and (20
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Query Match
Best Local Similarity 59.0%; Score 46; DB 18; Length 494;
Best Local Similarity 55.6%; Pred. No. 1.19e+02;
Matches 5; Conservative 3; Mismatches 1; Indels
Db 232 gpgqafql 240
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4 SXQEOTFQL 12
Search completed: Wed Dec 3 10:06:57 1997
Job time 8 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:44:39 1997; MasPar time 2.99 Seconds 135.144 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-2 (1-14) from US08915004.pep 78 1 XQHSXQEQTFQLXK 14 Itle: Description: Perfect Score:

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Scoring table:

91006 seqs, 28888923 residues PAM 150 Gap 15 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:ann 2:ann 3:ann 4:ann 5:unann 5:unann 7:unann 8:unann 9:unann 10:unann 12:unann 13:unann 13:unann 14:unann 10:15:unann 16:unrev pir51 Database:

Mean 22.756; Variance 33.196; scale 0.686 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Source Match Length DB ID Description No. Score Match Length DB ID Description 1 55 70.5 585 13 158403 gene H4(D10S170) pro 2 53 67.9 638 4 WIMM51 E1 protein - human p 3 53 67.9 1893 12 83543 peye development prot 5 52 66.7 113 12 833723 nuclear receptor pro 6 52 66.7 113 12 833723 cdysone-inducible p 8 51 65.4 450 3 A49733 involucrin - ring-ta 9 51 65.4 651 8 835505 E1 protein - human p 10 50 64.1 1458 7 A49707 phospholipase A2 rec 11 49 62.8 245 6 B33956 methylgalactoside pe 12 49 62.8 245 6 B33956 methylgalactoside pe 13 48 61.5 139 14 835357 T-cell receptor delt 14 48 61.5 387 3 A49774 involucrin - western 15 48 61.5 387 3 A49377 involucrin - mouse 16 48 61.5 755 9 B41836 amine oxidase (flavi 18 48 61.5 755 9 B41836 amine oxidase (flavi 19 48 61.5 786 8 B49349 probable succinedy		Pred. No	1.44e+00	3.38e+00	3.38e+00	3.38e+00	5.14e+00	5.14e+00	5.14e+00	7.78e+00	7.78e+00	1.17e+01	1.75e+01	1.75e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	3.87e+01
Ouery Score Match Length DB 55 70.5 585 13 53 67.9 634 4 53 67.9 638 8 52 66.7 113 12 52 66.7 113 12 52 66.7 113 12 51 66.7 13 12 51 65.4 450 3 51 65.4 450 3 64.12 65.4 450 3 64.12 65.4 450 3 64.12 65.4 450 3 64.13 1458 7 86.15 139 14 86.15 139 14 86.15 139 14 86.15 755 9 48 61.5 755 9 48 61.5 786 8		Description		El protein - human p		eye development prot	nuclear receptor pro		ecdysone-inducible p	involucrin - ring-ta	El protein - human p	phospholipase A2 rec	tyrocidine synthetas	methylgalactoside pe	T-cell receptor delt	, ,	•	١	oxidase	oxidase	protein -	probable succinoglyc	hypothetical protein
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AL TONMENTS

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RESULT 1 ENTRY TITLE ORGANISM DATE	I58403 #type complete gene H4(D10S170) protein - human #formal_amme Homo sapiens #common_name man 02-711-1996 #sequence revision 00-711-1996 #text change
ACCESSIONS REFERENCE	. 9
#authors	<pre>Grieco, M.; Cerrato, A.; Santoro, M.; Fusco, A.; Melillo, R.M.; Vecchio, G.</pre>
#journal #title	Oncogene (1994) 9:2531-2535 Cloning and characterization of H4 (D10S170), a gene involved in RET rearrangements in vivo.
#accession ##status ##molecul	IS Lty
##residues ##Cross-re GENETICS	##residues 1-585 ##label RES ##cross-references GB:S72869; NID:9633869; CDS_PID:9633870 CS
#note SUMMARY	gene name H4(D10S170) #length 585 #molecular-weight 65916 #checksum 4727
Query Match Best Local Si Matches 8	70.5%; Score 55; DB 13; Length 585; Similarity 61.5%; Pred. No. 1.44e+00; 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Db 161 qhleq	ghlegegefgvnk 173
Oy 2 OHSXQ	OHSXQEQTFOLXK 14
 RESULT 2	
 ENTRY	WIWL51 #type complete El protein - human papillomavirus type 51
 ORGANISM	type
#note DATE	host Homo saplens (man) 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 27-Tan-1905
ACCESSIONS REFERENCE	A40415 A40415
#authors	Lungu, O.; Crum, C.P.; Silverstein, S.J.
#journal #title	J. Virol. (1991) 65:4216-4225 Biologic properties and nucleotide sequence analysis of human
#cross-refer	papiliomavirus type 51. #cross-references MUID:91303675

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Primer-directed sequencing of human papillomavirus types.
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El protein - human papillomavirus type 26
#formal_name human papillomavirus type 26
20.Feb-1995 *sequence_revision 20.Feb-1995 *text_change
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03-Oct-1995
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#length 634 #molecular-weight 71684 #checksum 6865
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CLASSIFICATION #superfamily papillomavirus El protein
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46.2%; Pred. No. 3.38e+00;
vative 4; Mismatches 3; Indels
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Blochim. Blophys. Acta (1993) 1216:339-341
Brochim. novel Drosophila melanogaster genomic DNA fragment highly homologous to the DNA-binding domain of thyroid hormone-retinoic acid-vitamin D receptor subfamily.
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larity 54.5%; Pred. No. 5.14e+00;
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##molecule_type DNA
##residues 1-24
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To uning the terminal differentiation of keratinocytes, this protein if the terminal differences cross-linked to membrane proteins by transglutaminase and incorporated into an insoluble, cross-linked envelope under the plasma membrane.

FICATION #superfamily involucin confidence confidence cell envelope; duplication; epidermis; tandem
                                                                                                    Stone, B.L.; Thummel, C.S.
Cell (1993) 75:307-320
The Drosophila 78C early late puff contains E78, an
ecdysone-inducible gene that encodes a novel member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Cell (1988) 54:491-496
Remodeling of the involucrin gene during primate evolution.
A43733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       El protein - human papillomavirus type 30
#formal_name human papillomavirus type 30
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             involucrin - ring-tailed lemur
#formal_name Lemur qatta #common_name ring-tailed lemur
20-Feb-1993 #sequence_revision 23-Feb-1996 #text_change
                 #formal_name Drosophila melanogaster
03-May-1994 #sequence_revision 03-May-1994 #text_change
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                                                                                                                                                                                                                                                                      alternative splicing
#length 864 #molecular-weight 95792 #checksum 3050
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#length 450 #molecular-weight 50445 #checksum 4455
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                                                                                                                                                                                                                                                                                                                         Length 864;
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...hos 2; Indels
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Pred. No. 7.78e+00;
4; Mismatches 3; Indels
                                                                                                                                                                   nuclear hormone receptor superfamily.
                                                                                                                                                                                                                                                                                                                        Score 52; DB 12;
Pred. No. 5.14e+00
                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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                                                                                                                                                                                                                                      ##residues 1-864 ##label STO
##cross-references GB:U01087
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                                                                                                                                                                                                       preliminary
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atches 6; Consorting
     melanogaster)
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Best Local Similarity 46.2%;
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                                                   03-May-1994
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#domain fibronectin type II repeat homology #label 2FI\
#domain C-type lectin homology #label LCH
#length 1458 #molecular-weight 167199 #checksum 6528
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J. Bacteriol. (1989) 171:4881-4887
Gene cluster containing the genes for tyrocidine synthetases
I and 2 from Bacillus brevis: evidence for an operon.
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J. Biol. Chem. (1994) 269:1575-1578
Cloning and expression of a membrane receptor for secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrocidine synthetase (EC 6.-.-.) component 2 - Bacillus brevis (fragment)
submitted to the EMBL Data Library, August 1993
Primer-directed sequencing of human papillomavirus types.
$36505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A49707 #type complete
phospholipase A2 receptor precursor - rabbit
#formal_name Oryctolagus cuniculus #common_name domestic
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-May-1994 #sequence_revision 12-May-1994 #text_change
09-Sep-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *superfamily phospholipase A2 receptor; C-type lectin homology; fibronectin type II repeat homology glycoprotein; receptor; skeletal muscle; tandem repeat;
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23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change
                                                                                 ##molecule_type DNA
##residues 1-631 ##label DEL
##cross-references EMBL:X74474
CLASSIFICATION #superfamily papillomavirus El protein
KEYWORDS #superfamily protein
#length 631 #molecular-weight 71809 #checksum 8022
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                                                                                                                                                                                                                                                                                       Length 631;
                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                    Score 51; DB 8; Louis Pred. No. 7.78e+00;
                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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1-1458 ##label LAM
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CLASSIFICATION #superfamily phost
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#accession B33956
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Best Local Similarity 53.8%;
Matches 7; Conservative
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B33956
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A64000
Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Rirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirlay, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                  methylgalactoside permease ATP-binding protein (mglA) homolog - Haemophilus influenzae (strain Rd KW20) #formal_name Haemophilus influenzae 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Nov-1995
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#superfamily alpha-aminoadipyl-cysteinyl-valine synthetase;
acetate--CoA ligase homology; acyl carrier protein
homology; gramicidin S synthetase I repeat homology
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EMBO J. (1993) 12:715-724
Divergent evolution of T cell repertoires: extensive
diversity and developmentally regulated expression of the
Sheep gamma-delta T cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
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##note named as homolog to a protein from Escherichia coli
CLASSIFICATION #superfamily malk protein homology
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03 Feb-1994 #sequence_revision 03-Feb-1994 #text_change
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#domain malK protein homology #label MK2
#length 506 #molecular-weight 56567 #checksum 3128
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                                                                                                                                        Length 245;
                                                                                                                                                                                  1; Indels
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                                                                                                                                     Score 49; DB 6; Lt
Pred. No. 1.75e+01;
                                                                                                                                                                                  2; Mismatches
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                                                                                         #length 245 #checksum 6032
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##residues
                                                                                                                                     Query Match
Best Local Similarity 66.7%;
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Best Local Similarity 46.2%;
Matches 6; Conservative
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CLASSIFICATION
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#author
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DATE
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                                                                    KEYWORDS
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Djian, P.; Green, H.
Proc. Natl. Acad. Sci. U.S.A. (1991) 88:5321-5325
Involucrin gene of tarsioids and other primates: alternatives
in evolution of the segment of repeats.
A43704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               During the terminal differentiation of keratinocytes, this protein from the cytosol becomes cross-linked to membrane proteins by transglutaminase and incorporated into an insoluble, cross-linked envelope under the plasma membrane.

**TION **Superfamily involucrin cornified cell envelope; duplication; epidermis; tandem
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Mol. Biol. Evol. (1993) 10:1136-1149
The involucrin genes of the mouse and the rat: study of their
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#formal_name Tarsius bancanus #common_name western tarsier
20-Feb-1993 #sequence_revision 23-Feb-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Djian, P.; Phillips, M.; Easley, K.; Huang, E.; Simon, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation not shown; translated from GB/EMBL/DDBJ
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#length 387 #molecular-weight 45077 #checksum
                                                                                                                                                                                                                                      Score 48; DB 14; Length 139;
Pred. No. 2.61e+01;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 387;
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3; Mismatches 4; Indels
preliminary; translation not shown
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                                                                    ##residues 1-139 ##label HEI
##cross-references EMBL:212997
# #length 139 #checksum 4472
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##cross-references GB:M65124
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Local Similarity 46.2%;
les 6; Conservative
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                                    ##molecule_type mRNA
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3 07:57:39 1997

Wed Dec

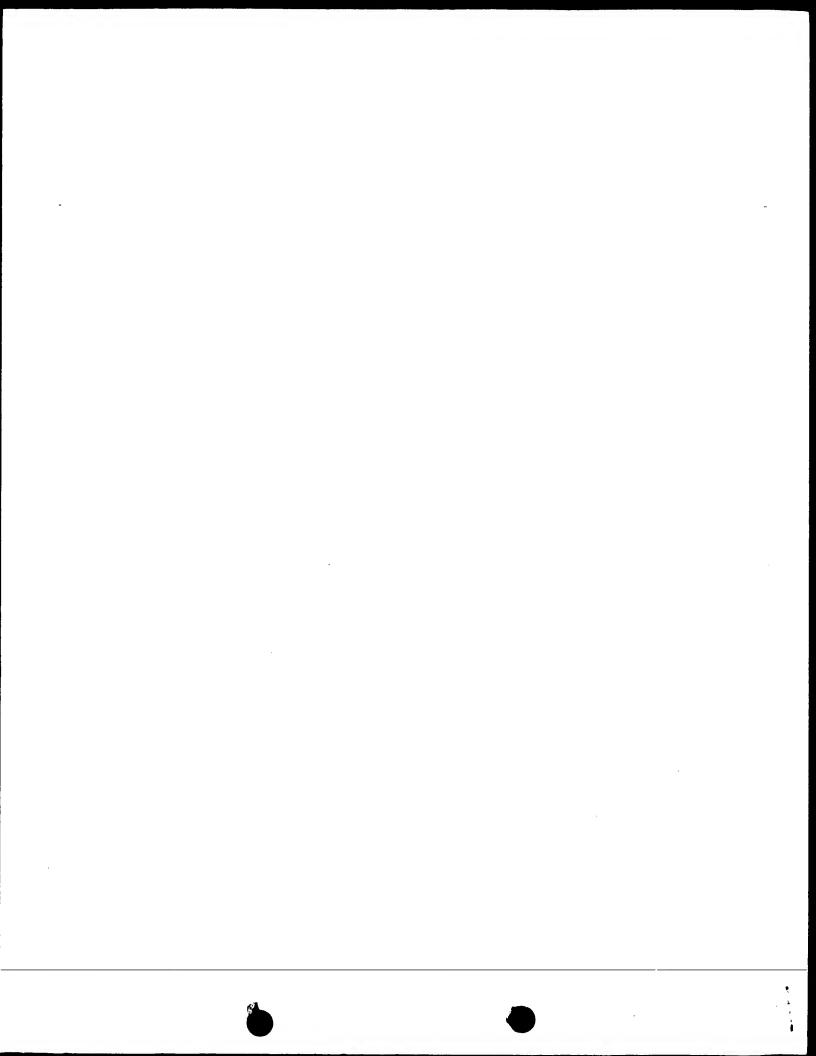
#superfamily involucrin cornified cell envelope; duplication; epidermis; tandem repeat #length 467 #molecular-weight 54919 #checksum 5202 CLASSIFICATION KEYWORDS SUMMARY

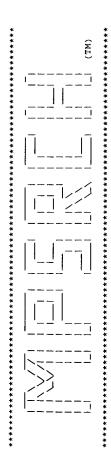
Query Match 61.5%; Score 48; DB 3; Length 467; Best Local Similarity 46.2%; Pred. No. 2.61e+01; Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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δy

Search completed: Tue Dec 2 14:44:51 1997 Job time: 12 secs.





Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:44:12 1997; MasPar time 2.03 Seconds 145.979 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-2 (1-14) from US08915004.pep 78 1 XQHSXQEQTFQLXK 14 Description: Perfect Score: tle:

Seguence:

PAM 150 Gap 15 Scoring table:

59021 seqs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot34 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11

Mean 23.758; Variance 28.025; scale 0.848 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Ollery					
No.	Score	Match	Match Length DB	DB	ΩI	Description	Pred. No
П	53	67.9	634	10	VE1_HPV51	REPLICATION PROTEIN E	7.11e-01
7	23	67.9	638	10	VE1_HPV26	REPLICATION PROTEIN E	7.11e-01
m	52	66.7	864	ო	E78A_DROME	ECDYSONE-INDUCIBLE PR	1.17e+00
4	51	65.4	450	Ŋ	INVO_LEMCA	INVOLUCRIN.	1.91e+0(
S	51	65.4	631		VE1_HPV30	REPLICATION PROTEIN E	1.91e+00
Ø	20	64.1	1458	7	PA2R_RABIT	180 KD SECRETORY PHOS	3.09e+0(
7	49	62.8	506		MGLA_HAEIN	GALACTOSIDE TRANSPORT	4.97e+00
ω	48	61.5	387	Ŋ	INVO_TARBA	INVOLUCRIN.	7.94e+00
σ	48	61.5	467	Ŋ	INVO_MOUSE	INVOLUCRIN.	7.94e+0(
10	48	61.5	629	10	VE1_HPV31	REPLICATION PROTEIN E	7.94e+0(
11	48	61.5	755	Н	AMO_KLEAE	AMINE OXIDASE PRECURS	7.94e+00
12	4 8	61.5	757	Н	AMO_ECOLI	COPPER AMINE OXIDASE	7.94e+0(
13	48	61.5	786	ო	EXOP_RHIME	SUCCINOGLYCAN BIOSYNT	7.94e+0(
14	47	60.3	335	σ	TRPD_BUCAP	ANTHRANILATE PHOSPHOR	1.26e+01
15	47	60.3	337	S	KAPC_ASCSU	CAMP-DEPENDENT PROTEI	1.26e+01
16	47	60.3	426	თ	TEF1_MOUSE	TRANSCRIPTIONAL ENHAN	1.26e+01
17	47	60.3	426	σ	TEF1_HUMAN	TRANSCRIPTIONAL ENHAN	1.26e+0]
18	47	60.3	570	Ξ	YNE3_CAEEL	HYPOTHETICAL 64.2 KD	1.26e+01
19	47	60.3	923	വ	HXK3_HUMAN	HEXOKINASE TYPE III (1.26e+0
20	46	59.0	154	~	AROD_ACTPL	3-DEHYDROQUINATE DEHY	1.98e+01
21	46	59.0	189	Ŋ	INA1_PIG	INTERFERON ALPHA-1 PR	1.98e+01
22	46	59.0	275	4	FRA1_RAT	FOS-RELATED ANTIGEN 1	1.98e+01

1.98e+01 1.98e+01 1.98e+01 1.98e+01 1.98e+01 1.98e+01 1.98e+01 1.98e+01 1.98e+01 1.98e+01 3.09e+01 3.09e+01 3.09e+01 3.09e+01 3.09e+01 3.09e+01	
CYTOCHROME P450 IIA6 ALKALINE PHOSPHATASE, ALKALINE PHOSPHATASE, ALKALINE PHOSPHATASE, ALKALINE PHOSPHATASE, ALKALINE PHOSPHATASE, ALKALINE PHOSPHATASE, REPLICATION PROTEIN E NUCLEOPORIN NUP82 (NU AMP DEAMINASE 1 (EC 3) PROSTATE SPECIFIC MEM REVERSE GYRASE (CONTA SUPPRESSOR OF TOXICIT HYPOTHETICAL 13.9 KD ESSI PROTEIN (PROTESS GLC OPERON TRANSCRIPT SEGMENTATION POLARITY TRANSCRIPTIONAL BHAN CDC4-LIKE PROTEIN (FR TISSUE PLASMINOGEN AC HYPOTHETICAL 86.1 KD RETROTHED PO	ж.
CPA6_HUMAN PPB2_HUMAN PPB1_HUMAN PPB1_HUMAN PPB1_HUMAN NUB2_ERSAT AWD1_HUMAN PPB1_HUMAN PPB1_HUMAN NUB2_ERSAT AWD1_HUMAN POPG_ECOLI PRACSUCCECOLI ESS1_ERSAT URC_ECOLI ESS1_CRAST URC_ECOLI URC_ECOL	PTP2_HUMAN
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ALIGNMENTS

HUMAN PAPILLOMAVIRUS TYPE 26. VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES. LESULT 2 STANDARD; PRT; 638 AA.

C P36722; D 1017W-1994 (REL. 29, CREATED)

T 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)

O1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

REPLICATION PROTEIN E1. [1] SEQUENCE FROM N.A. MEDLINE; 94265501. RESULT

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C -1 DEVELOPMENTAL STAGES WILLST THE SHORTER FORM, E78B, IS EXPRESSED ONLY
IN MID-PUPAL STAGES, WHILST THE SHORTER FORM, E78B, IS MAXIMALLY
EXPRESSED IN NEWLY FORMED PREPUPAL.

-1 INDUCTION: BOTH FORMS REQUIRE ECDYSONE FOR ACTIVITY. E78B ALSO
REQUIRES ECDYSONE-INDUCED PROTEINS FOR MAXIMAL EXPRESSION.

-1 ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF PROTEIN E78 ARE
PROBABLY PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.

-1 SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC

NUCLEAR HORWONE RECEPTORS.

REMBL; VA73045; E74981; --

REMBL; X73045; E178G.

REMBL; X73045; E178C.

REMBL; X73045; STEROID_FINGER.

REMBL; X73045; STEROID_FINGER.
                                                                                                                                                                                      ô
          CURR. TOP. MICROBIOL. IMMUNOL. 186:13-31(1994).
-!- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR DNA REPLICATION.
-!- SUBCELLULAR LOCATION: NUCLEAR.
EMBL. X74472 (396959).
-!- S18546; S36546.
EARLY PROTEIN; DNA REPLICATION; HELICASE; ATP-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MARTÍN-BLANCO E., KORNBERG T.B.;
BIOCHÍM. BIOPHYS. ACTA 1216:339-341(1993).
-!- FÍUNCTION: INDUCES THE EARLY LATE PUFF 78C WHICH TRIGGERS PUPARIUM
FORMATION AND DEVELOPMENT.
-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
                                                                                                                                                                                      Gaps
                                                                                                                                                                                      ö
                                                                                                                                                       Query Match 67.9%; Score 53; DB 10; Length 638; Best Local Similarity 46.2%; Pred. No. 7.11e-01; Matches 6; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4-TYPE ZINC FINGERS (TWO)
                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA
                                                                                                                ATP (POTENTIAL). ; 6E36534F CRC32;
                                                                                                                                                                                                                                                                                                                          01-NQY'1995 (REL. 32, CREATED)
01-NQY-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ECDYSONE-INDUCIBLE PROFEIN E78-A (DR-78).
                                                                                                                                                                                                                                                                                                     864 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-SER.
POLY-GLN.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-GLN.
POLY-SER.
POLY-ASN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-GLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-SER
                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     DROSOPHILA MELANOGASTER (FRUIT FLY)
                                                                                                                            71956 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 321-433 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STONE B.L., THUMMEL C.S.;
CELL 75:307-320(1993).
                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                474
                                                                                                                                                                                                                ehsfddatfdlsk 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432
427
427
427
1088
202
2247
2247
315
333
333
333
335
335
335
DELIUS H., HOFMANN B.;
                                                                                                                                                                                                                                           OHSXQEQTFOLXK 14
                                                                                                                             638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CANTON-S;
MEDLINE; 94006562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94060116.
                                                                                                                467
                                                                                                                                                                                                                                                                                                                                                                                      EIP78C OR E78A.
                                                                                                                                                                                                                                                                                                    E78A DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC-FINGER
                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
                                                                                                                NP_BIND
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                                                                                                                                                                                                                337
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VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES.
                             MISSING (IN TRUNCATED FORM E78B).
QLQQQQQHQQQ -> SCNSSSTSSR (IN REF. 2).
AGMS -> VGMK (IN REF. 2).
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 92407963.
CHAN S.Y., BERNARD H.U., ONG C.K., CHAN S.P., BIRGIT H., DELIUS H.;
                                                                                                                                                                                                                                                  LEMUR CATTA (RING-TAILED LEMUR).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.4%; Score 51; DB 5; Length 450; Best Local Similarity 46.2%; Pred. No. 1.91e+00; Matches 6; Conservative 4; Mismatches 3; Indels
                                                                               Score 52; DB 3; Length 864;
                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE, 94265501.
CURR. TOP. MICROBIOL. IMMUNOL. 186:13-31(1994).
                                                                                        Pred. No. 1.17e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                               50445 MW; BB1B0C73 CRC32;
                                                          5EEB72C0 CRC32;
                                                                                                                                                                                                 01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEL_HPV30 STANDARD; PRT; 631 AA. 005112; 01-FEB-1994 (REL. 29, CREATED) 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE) REPLICATION PROTEIN E1.
                                                                                                                                                                                450 AA.
                                                                                                  3; Mismatches
           POLY-GLN
                     POLY-ASN
486
500
554
7474
331
95865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 358-409 FROM N.A.
                                                                             66.7%;
Similarity 54.5%;
6; Conservative
                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 ggapgegelhlgk 163
                                                                                                                                                                                                                                                                                                          TSENG H., GREEN H.;
CELL 54:491-496(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QHSXQEQTFQLXK 14
                                                                                                                     333 qhpqqqqsfgl 343
                                                                                                                                       2 QHSXQEQTFQL 12
                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             450 AA;
                                                           864 AA;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 88295123.
 4481
4490
546
1
321
430
                                                                                                                                                                      LT 4
INVO_LEMCA
P14590;
                                                                                                                                                                                                                               INVOLUCRIN.
                   DOMAIN
VARSPLIC
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                          SEQUENCE
                                                                               Query Match
                                                 CONFLICT
 DOMAIN
          DOMAIN
                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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J. VIROL. 66:5714-5725(1992).

-:- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR DNA REPLICATION.

-:- SUBCELLCULAR LOCATION: NUCLEAR.

EMBL; X744/4; G334093; -.

PIR; S36505; S36505.

BARLY PROTEIN, DNA REPLICATION; HELICASE; ATP-BINDING;

NUCLEAR PROTEIN.

459 466 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                              LAMBEAU G., ANCIAN P., BARHANIN J., LAZDUNSKI M.;
J. BIOL. CHEM. 269:1575-1578 (1994).
-!- FUNCTION: MAY HAVE A KEY ROLDE IN NORMAL AND PATHOLOGICAL ACTIONS
OF SECRETORY PHOSPHOLIPASE A2. ALSO BINDS TO SNAKE PA2-LIKE
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: LUNG, SKELETAL MUSCLE, BRAIN, KIDNEY AND
                                                                                                                                                                                                                                                                  01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R).
0RYCTOLAGUS CUNICLUS (RABITY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
180 KD SECRETORY PHOSPHOLIPASE A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, U03455; G456376; -. SIGNAL; REPEAT; GLYCOPROTEIN; LECTIN.
                                                                                                                                                    ö
                                                                                                                            65.4%; Score.51; DB 10; Length 631; 53.8%; Pred. No. 1.91e+00; vative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORM).
FORM).
FORM).
FORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL). CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-TYPE LECTIN 1 (LONG FO
C-TYPE LECTIN 3 (LONG FO
C-TYPE LECTIN 3 (LONG FO
C-TYPE LECTIN 5 (LONG FO
C-TYPE LECTIN 5 (LONG FO
C-TYPE LECTIN 7 (LONG FO
C-TYPE LECTIN 7 (LONG FO
C-TYPE LECTIN 8 (LONG FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-II
                                                                                            459 466 ATP (POTENTIAL).
631 AA; 71809 MW; 753395D7 CRC32;
                                                                                                                                                                                                                                               PRT; 1458 AA.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 94124484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   981
1054
1106
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1458
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1416
1416
1658
1658
3250
3250
798
1098
1098
1376
1376
1376
408
471
725
725
                                                                                                                                                                           329 qhsfqdcqfelsk 341
                                                                                                                                                                                                 2 OHSXQEQTFOLXK 14
                                                                                                                                                                                                                                                                                                                                         EUTHERIA; LAGOMORPHA.
                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   981
1054
1106
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                                                                                                                                                                                                                                               PAZR_RABIT
P49260;
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CARBOHYD
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TRANSMEM
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                                                                                                        SEQUENCE
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                                                                                                                               Query Match
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                                                                                                                                                     Matches
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'NEWTER J.C.;

SCIENCE 269:496-512(1995).

SCIENCE 269:496-512(1995).

C -: FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM

THE TRANSPORT SYSTEM (BY SIMILARITY).

CC -: SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED (POTENTIAL).

CC -: SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY

CC -: SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY

CC EMBL; L45461; G1005849; -.

DR EMBL; L45461; G1005849; -.

DR EMBL; U37764; G922867; -.

DR EMBL; U37764; G922867; -.

DR FRANSPORT; SGGAR TRANSPORTER.

FT RANSPORT; SGGAR TRANSPORT: INNER MEMBRANE; ATP-BINDING.

FT RANSPORT; SGGAR TRANSPORT; INNER MEMBRANE; ATP-BINDING.

FT SEQUENCE 506 AA; 56567 WW; 8964ECA2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                HAEMOPHILUS INFLUENZAE.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLEIGCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., RELIGAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M., MCKENNEY, K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., FITZHORAN J.E., FURMENDAN B.C., GOGGRAGEN N.S.M., BRANDON R.C., FITZHAMAN J.L., FUHRMANN J.L., FUHRMANN J.L., FUHRMANN J.L., FUHRMANN J.L., FUHRMANN J.L., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TARSIUS BANCANUS (WESTERN TARSIER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó;
                                                                                                                                     .;
0
                                                                                               Score 50; DB 7; Length 1458;
Pred. No. 3.09e+00;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 6; Length 506;
Pred. No. 4.97e+00;
3; Mismatches 4; Indels
                                                    POTENTIAL.
MW; FA57C2CA CRC32;
                                                                                                                                                                                                                                                                                                          01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
MGLACTOSIDE TRANSPORT ATP-BINDING PROTEIN MGLA.
MGLA OR HI0823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 AA
                                                                                                                                                                                                                                                                           506 AA.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
1121 1121
1130 1130
1319 1319
1439 1439
1458 AA; 167199 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 62.8%;
Local Similarity 46.2%;
les 6; Conservative
                                                                                                     Query Match 64.1%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                       849 hsaheqefilsk 860
                                                                                                                                                                                             3 HSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PASTEURELLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVO_TARBA
P24711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INVOLUCRIN
                                                                                                                                                                                                                                                                         MGLA_HAEIN
                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
     CARBOHYD
                                                      CARBOHYD
                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                             P44884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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     SETTE
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VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           757 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 31-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H(2)O(2).
-!- COFACTOR: COPPER AND TOPAQUINONE.
-!- SUBCELLULAR LOCATION: PERIPLASMIC.
                                                                                                                                                                                                                                                464 A'
71227 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83576 MW;
                                                                                                                                                                                                                                                                                                            y Match
Local Similarity 54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 50.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 qsgldqtfqvek 121
                                                                                                                                                                                                                                                                                                                                                                                   327 qhsfndttfdl 337
                                                                                                                                                                                                                                                                   629 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        2 QHSXQEQTFQL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 HSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      755 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 92210491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAOA OR IYNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOPAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 11
AMO_KLEAE
P49250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=W70
                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMO_ECOLI
P46883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                            Query Match
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                                                                         DJIAN P., GREEN H.;
PROC. NATL. ACAD. SCI. U.S.A. 88:5321-5325(1991).
-!- FUNCTION: INVOLCERIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEARS
IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO
MEMBRANE PROTEINS BY TRANSGLUTAMINASE. ALL THAT RESULTS IN THE
FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE.
-!- TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND
GTHER STRAITFIED SQUAMOUS EPITHELIA.

GTHER STRAITFIED SQUAMOUS EPITHELIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOL. BIOL. EVOL. 10:1136-1149(1993).

-!- FÜNCTION: INVOLUCRIN IS A KERATTNOCYTE PROTEIN THAT FIRST APPEARS IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO MEMBRANE PROTEINS BY TRANSCLOTAMINASE. ALL THAT RESULTS IN THE FÜRMATION OF AN INSOLUBLE BENVELOPE BENEATH THE PLASMA MEMBRANE.

-!- TİSSÜLE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND EMBL: | L28819; 6454419;

EMBL: | L28819; 6454419;
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DJIAN P., PHILLIPS M., EASLEY K., HUANG E., SIMON M., RICE R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHEŖIA; ROĐENTIA.
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                                                                                                                                                                                                                                                                                                                                      Score 48; DB 5; Length 38/;
Pred. No. 7.94e+00;
....matches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 5; Length 467; Pred. No. 7.94e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                387 AA; 45077 MW; 2800B15B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54919 MW; 39DCOAFE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
INVOLUCRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                         PIR; A43704; A43704.
PROSITE; PS00795; INVOLUCRIN.
KERATINOCYTE; REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E1.
HUMAN PAPILLOMAVIRUS TYPE 31.
                                                                                                                                                                                                                                                                                                                                                        / Match
Local Similarity 46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 46.2%;
                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INVO_MOUSE STANDARD; P48997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPLICATION PROTEIN E1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE).
  [1] |
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                           MEDLINE; 91271381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NIH SWISS;
MEDLINE; 94104476
                                          TISSŲE=LIVER;
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VE1_HPV31
P17382
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        ery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                  235
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MEDLINE; 89299478.
MEDLINE; 89299478.
GOLDSBOROUGH M.D., DISLLVESTRE D., TEMPLE G.F., LORINCZ A.T.;
VIROLOGY 171:306-3311(1989).
-1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR DNA REPLICATION.
-1- SUBCELLULAR LOCATION: NUCLEAR.
EMBL; 004353; G459918; -.
PIRI: CIRCALION.
PIRI: CIRCALION.
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUGINO H., SASAKI M., AZAKAMI H., YAMASHITA M., MUROOKA Y.;
J. BACTERIOL. 174:2485-2492(1992).
-!- FUNCTION: ACTIVE ON TYRAMINE, TRYPTAMINE, BETA-PHENETHYLAMINE AND
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) = RCHO + NH(3) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
01-MINE OXIDASE PRECURSOR (EC 1.4.3.6) (MONAMINE OXIDASE) (TYRAMINE
                                                                                                                                                                                                                                                                                                                                                                                                             ó
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CATALYTIC BASE (BY SIMILARITY).
TOPAQUINONE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                         Length 629;
                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 1; Length 755; Pred. No. 7.94e+00; 3; Mismatches .3; Indels
                                                                                                                                                                                                                EARLY PROTEIN; DNA REPLICATION; HELICASE; ATP-BINDING; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- INDUCTION: BY TYRAMINE.
-i- SIMILARITY: TO OTHER COPPER/TOPAQUINONE OXIDASES.
EMBL: D10208; G216723; -.
OXIDOREDUCTASE: COPPER; TPQ; PERIPLASMIC; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPPER (POTENTIAL).
COPPER (POTENTIAL).
COPPER (POTENTIAL).
4; 735E26ED CRC32;
                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 10;
Pred. No. 7.94e+00;
                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
DA96E287 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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SEQUENCE FROM N.A.
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                                                                                                                                                                                            STRAIN=K12 / W3110;
AZAKAMI H., YAMASHITA M., ROH J.H., SUZUKI H., KUMAGAI H., MUROOKA Y.;
J. FERMENT. BIOENG. 77:315-319(1994).
                                                                                                              PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) = RCHO + NH(3) +
                                                                                                                                                                                                                                                                                     STRAIN=K10;
MEDLINE: 96164434.
PARSONS M.R., CONVERY M.A., WILMOT C.M., YADAV K.D.S., BLAKELEY V., CORNER A.S., PHILLIPS S.E.V., MCPHERSON M.J., KNOWLES P.F.;
STRUCTURE 3:1171-1184(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
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   01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 33, LAST SEQUENCE UPDATE)
01-EPB-1996 (REL. 33, LAST ANNOTATION UPDATE)
COPPER AMINE OXIDASE PRECURSOR (EC 1.4.3.6) (TYRAMINE OXIDASE)
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
COPPER AMINE OXIDASE.
CATALYTIC BASE (PROBABLE).
TOPAQUINONE.
                                                                                                                                                                                                                                                                                                                                                                                                                  -:- COFACION: COPPER AND TOPAQUINONE.
-:- SUBGUIT: HOMODIMER.
-:- SUBCELLULARITY: TO OTHER COPPER/TOPAQUINONE OXIDASES.
EMBL: D23670; G809499; --
EMBL: L47571; G1000851; --
ECCOENE: B613139; TYNA.
OXIDOREDUCTASE; COPPER; TPQ; PERIPLASMIC; SIGNAL.
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01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOFATION UPDATE)
SUCCINOGINCAN BIOSYNTHESIS TRANSPORT PROTEIN EXOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K -> E (IN REF. 1).

GY -> VI (IN REF. 1).

I -> II (IN REF. 1).

MISSING (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P -> I (IN REF. 1).
A -> P (IN REF. 1).
H -> D (IN REF. 1).
7; 1223C5B7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 1; Le
Pred. No. 7.94e+00;
3; Mismatches 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COPPER
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Conservative
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659
757 AA;
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Matches 6; Conser
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                                                                                                                                      ENTEROBACTERIACEAE
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                   ESCHERICHIA COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHIZOBIACEAE
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                                                                               MAOA OR TYNA
                                                                                                                                                                                                                                                                                                                                                                                                        H(2)0(2)
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CONFLICT
SEQUENCE
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BINDING
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CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (EC 2.7.1.37) (PKA C).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUNSON M.A., BAUMANN P.; SUBMI/GENBANK/DDBJ DATA BANKS.
SUBMITTED (DEC-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
I. CATALYIT ACTIVITY: ANTHRANILATE + PHOSPHORIBOSTLPYROPHOSPHATE .
N.S. +PHOSPHORIBOSYL-ANTHRANILATE + PYROPHOSPHATE.
I. PATHWAY: SECOND SIEP IN BIOSYNTHESIS OF TRYPTOPHAN.
EMBL; Z19055; G396656; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASCARIS SUUM (PIG ROUNDMORM) (ASCARIS LUMBRICOIDES).
EUKARYOIA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; ASCARIDIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                       BECKER A., KLEICKMANN A., KELLER M., ARNOLD W., PUEHLER A.;
MOL. GEN. GENTT. 241:367-379(1993).
-!- PATHWAY: EXOPOLYSACCHARIDE BIOSYNWHESIS.
-!- PATHWAY: LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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TRYPTOPHAN BIOSYNTHESIS; TRANSFERASE; GLYCOSYLIRANSFERASE.
SEQUENCE 335 AA; 38090 MW; 74288035 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB 3; Length 786;
Pred. No. 7.94e+00;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 9; Length 335; Pred. No. 1.26e+01; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOYATION UPDATE)
ANTHRANILATE PHOSPHORIBOSYLLTRANSFERASE (EC 2.4.2.18).
                                                                                                                                                                                                                                                                                                                                                                                                                EXOPOLYSACCHARIDE SYNTHESIS; TRANSPORT; TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; UNCERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         786 AA; 86123 MW; A45B9144 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 AA
STRAIN-1021;
MEDLINE; 94042870.
GLUCKARNIN M.A., REUBER T.L., WALKER G.C.;
J. BACTERIOL. 175:7045-7055(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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ilarity 30.8%; F
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.3%;
Best Local Similarity 55.6%;
                                                                                                                                                                                                                                                                                       EMBL, L20758; G393241; -.
EMBL, 222636; G605655; -.
PIR; B49349; B49349.
PIR; S37031; S37031.
PIR; S39960; S39960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 QHSXQEQTFOLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BUCHNERA APHIDICOLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 OEQTFOLXK 14
                                                                                                                                                                  MEDLINE; 94067019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 15
KAPC_ASCSU
P49673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 14
TRPD_BUCAP
P42392;
                                                                                                                                                STRAIN-2011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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29 ? PROTEIN KINASE.
35 43 ATP (BY SIMILARITY).
58 58 ATP (BY SIMILARITY).
152 152 BY SIMILARITY.).
337 AA; 39171 MW; EDA30BB3 CRC32;
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lery Match 60.3%; Score 47: DB 5; Length 337; est Local Similarity 53.8%; Pred. No. 1.26e+01; Matches 7; Conservative 0; Mismatches 6; Indels Search completed: Tue Dec 2 14:44:21 1997 Job time : 9 secs. 47 ghrasegyfalkk 59 || || || || 2 | QHSXQEQTFOLXK 14 47 g ò

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:46:34 1997; MasPar time 2.02 Seconds 73.024 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-3 (1-12) from US08915004.pep 94 Perfect Score: Description: tle:

1 XIRFLHSFTMYK 12 sedneuce:

PAM 150

Scoring table:

101610 seqs, 12294212 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

i.parri 2.part2 3.part3 4.part4 5.part5 6.part6 7.part7 8.part8 9.part9 10.part10 11.part11 12.part12 13.part13 14.part14 15.part15 16.part16 17.part17 18.part18 19.part19 20.part20 21.part21 a-geneseq28 Database:

Mean 18.812; Variance 62.835; scale 0.299 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

(æ					
ult No.	Score	Query Match	Length	DB	đ	Description	Pred. No.
-	94	100.0	12	20	R99923	Osteoclastogenesis in	5.77e-03
2	94	100.0	326	70	R99940	Mutated OCIF, OCIF-DD	5.77e-03
· (*)	94	100.0	327	20	R99941	Mutated OCIF, OCIF-DD	5.77e-03
4	94	100.0	359	20	R99939	Mutated OCIF, OCIF-DC	5.77e-03
· CO	94	100.0	359	20	R99937	Mutated OCIF, OCIF-DC	5.77e-03
· vc	94	100.0	360	20	R99936	Mutated OCIF, OCIF-DC	5.77e-03
7	94	100.0	360	20	R99938	Mutated OCIF, OCIF-DC	5.77e-03
- α	94	100.0	380	20	R99924	Mature osteoclastogen	5.77e-03
σ	94	100.0	393	20	R99948	Mutated OCIF, OCIF-CB	5.77e-03
101	94	100.0		20	R99942	Mutated OCIF, OCIF-CL	5.77e-03
2-	76	100.0	401	20	R99934		5.77e-03
12	76	100.0	401	20	R99932	Mutated OCIF, OCIF-C2	5.77e-03
1 1-	46	100.0	401	20	R99935		5.77e-03
14	76	100.0	401	20	R99931	Mutated OCIF, OCIF-C1	5.77e-03
	9.6	100.0	401	20	R99925	Full length osteoclas	5.77e-03
9 4	92	97.9	401	20	R99933	Mutated OCIF, OCIF-C2	9.54e-03
17	0	63.8	11	11	R56496	TATA-binding protein-	2.11e+01
8 -	56	59.6			R05420	bt4 Gene encoding Bt4	5.18e+01
6	56	59.6		7	R10129	Lepidopteran-active t	5.18e+01
20		59.6	1165	~	R08200	bt4 Protoxin gene pro	5.18e+01

5.18e+01 5.18e+01	5.18e+01 8.06e+01	8.06e+01	8.06e+01	1.25e+02	55e+0	1.55e+02	1.55e+02	1.92e+02	1.92e+02	2.37e+02	2.37e+02	2.37e+02	2.37e+02	•	.3	'n,	•	2.37e+02	۳;	"	.37e+0	2.37e+02
Incecticidal crystal Bt4 protoxin.	Delta endotoxin. Bacillus subtilis srf	anoce	Sequence of a polypep	i.	Conglutinin.	C	N-heparan sulphate su	Biotin-sypthase gene	Biotin synthetase (Bi	Oncostatin M deletion	Oncostatin M subtitut	Human oncostatin M.	Luciferase mutant Tyr	Recombinant luciferas	Luciferase of Hotaria	Thermostable lucifera	Luciferase.	Firefly luciferase re	Vaccinia virus vector	Lux::npt-II fusion pr	Hamster sulphonylurea	Rat sulphonylurea rec
24	R39756 R34720	R79502	R49726	R10098	R12222	R75642	R43959	P70328	P81191	R12899	R12897	R88202	R14121	P94367	R84178	R33709	R05788	R50011	R72801	R28127	R77085	R77087
13.2	∞ /	14	σ	7	m	15	œ	~	Н	ო	m	17	m	ч	16	ø	Ŋ	σ	13	Ŋ	14	14
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59.6 59.6	٠. ^۲	57.4	~	55.3	-+		54.3	æ.	e.	\sim	2	Α.	α	ď	ď		ď		2	52.1	52.1	52.1
56 56			54	52	51	51	51	20	20	49	9	49	49	49	49	49	49	4	49	49	49	49
21	23	25	26	27	28	53	30	31	32	33	34	35	36					4	4	43	44	4.5

ALIGNMENTS

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22-APR-1997 (first entry)
Osteoclastogenesis inhibitory factor peptide fragment #3.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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WALL SOURCE AND STANDARD TO SECOND STANDARD STANDARD SECOND STANDARD SECOND STANDARD SECOND STANDARD SECOND STANDARD SECOND 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-1996; JO0374.
21-GFB-1995; JP-207508.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(GOLO M, Higashlo K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                            Location/Qualifiers
.T
R99923 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                        /note= "Any amino acid" w09626217-A1.
                                                                                                                                                                                                                                                                                                                                        Misc_difference 1
                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                            osteoporosis
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RESULT
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Gaps . 0 Length 12; Score 94; DB 20; Length 12; Pred. No. 5.77e-03; 0; Mismatches 0; Indels Match 100.0%; Local Similarity 100.0%; les 11; Conservative 2 irflhsftmyk 12 Query Match Matches

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2 IRFLHSFTMYK 12 ò

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RESULT

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N-PSDB; T33171
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                                                                                                                                                                                                                                                                  Foundation obtained by the interior of the interior of obtained onto control, esp. treatment of osteoporosis for hone resorption control, esp. treatment of osteoporosis claim 56. Page 113-114; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents ociF-DDD1 in which amino acids 178-252 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kb under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                          Ostepclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutated OCIF, OCIF-DDD2.''
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morinaga T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Maltch 100.0%; Score 94; DB 20; Length 326; Best Local Similarity 100.0%; Pred. No. 5.77e-03; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9bzyw_
29-AuG-1996.
20-AuG-1996; J00374.
R 20-FEB-1995; JP-054977.
R 21-Juμ-1995; JP-207508.
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
PI GOLO M, Higashio K, Kobayashi F, Mochizuki S, Mor
PI GOLO M, N. Shima N, Tsuda E, Ueda M, Yano K, Ya
                                                                                                                                                                            20-FEB-1996; JO0374.
20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
SNOW SNOW BRAND MILK PROD CO LID.
Goto |M. Higashio K, Robayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33170.
                                                                                                                                Aisc_difference 198..199
/note= "Positition of deletion, delta 178-252"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc_difference 273..274
/note# "Positition of deletion, delta 253-326"
                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
R99940 standard; Protein; 326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R9994 standard; Protein; 327 AA.
                     23-APR-1997 (first entry)
Mutated OCIF, OCIF-DDD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                              22..326
/note= "Mature OCIF-DDD1"
/isc|different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein 22..327
/note= "Mature OCIF-DDD2"
                                                                                           1..21
"Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..21 "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 AA;
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                                                         osteóporosis.
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23-APR-1997
                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 59; Page 115-116; 183pp; Japanese.
This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DDD2 in which amino acids 253-326 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions: The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natural 193109.

Natural 193109.

Natural 193109.

To bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis for sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR4 in which amino acids 123-164 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 94; DB 20; Length 327;
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 359;
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20-FEB-1995; JP-054897.
21-UL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein 22.359
/note= "Mature OCIF-DCR4"
Misc_difference 143..144
/note= "Positition of deletion, delta 123-164"
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Pred. No. 5.77e-03;
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Local Similarity 100.0%;
les 11; Conservative
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 irflhsftmyk 305
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                                                                                                                                                                                                                                                                                                                                                                                                   osteoporosis
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Matches
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2 IRFLHSFTMYK 12

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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 47, Page 107-109; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR2 in which amino acids 43.84 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1997 (first entry)
Mutated OCIF, OCIF-DCR1.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                        Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                   20-FEB-1995; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOCD M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-40230/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 94; DB 20; I
Pred. No. 5.77e-03;
0; Mismatches 0;
                                                                                                                                                                                                Misc_difference 63..64
/note= "Position of deletion, delta 43-84"
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Mote- Mature OCIF-DCR1"

Msc_difference 22.7

Anote- "Position of deletion, delta 2-42"
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                                                                                                                        Location/Qualifiers
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r
R99937 standard; Protein; 359 AA.
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                                            23-APR-1997 (first entry) Mutated OCIF, OCIF-DCR2.
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29-AUG-1996.
20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
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                                                                                                                                                                    Protein. 22.359 /note= "Mature OCIF-DCR2"
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/note= "Signal peptide"
                                                                                                                                                     "Signal peptide"
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                                                                                             osteoporosis
                                          23-APR-1997
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                                                                                                            Synthetic.
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                                                                                                                                        Peptide
                                                                                                                                                          /note=
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Matches
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Morinaga T; Yasuda H;

Gaps .. O

Length 359; 0; Indels

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Introduce to select a stogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 50. Page 109-111, 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR3 in which amino acids 85-122 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of disorders of bone resorption, e.g.
                                                                                                                          ON encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 44; Page 105-107; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR1 in which amino acids 2-42 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C. deg.C. or 10 mins at 56 deg.C. deg.C. or 10 mins at 56 deg.C. or 10 mins at 60 deg.C. or 60 mins at 60 deg.C. or 60 deg.C. or 60 deg.C. or 60 deg.C. or 60 
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Mutated OCIF, OCIF-DCR3.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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                                Morinaga T;
Yasuda H;
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Pred. No. 5.77e-03;
0; Mismatches 0; Indels
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20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOCO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, H1gashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shina N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
N-PSDB; T33166.
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/note= "Signal peptide"
Protein 22..360
/note= "Mature OCIF-DCR3"
Misc_difference 105..106
/note= "Position of deletion, delta 85-122"
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Best Local Similarity 100.0%;
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N-PSDB; T33168.
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Score 94; DB 20; Length 360; Pred. No. 5.77e-03;

Query Match Best Local Similarity 100.0%;

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Mature osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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            Gaps
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Yasuda H;
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Yasuda H;
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Pred. No. 5.77e-03;
0; Mismatches 0; Indels
       Indels
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20-FB-1996; JO0374.
20-FB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M. Higashio K, Kobayashi F, Mochizuki S, MPI, 96-402320,40.
WPI, 96-402320,40.
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20-FEB-1996; JP-054977.
21-JUL-1995; JP-207508.
21-JUL-1995; JP-207508.
GOTO M, Higashio K, Kobayashi F, Mochizuki S, Makaqawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI: 96-402320/40.
     Mismatches
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R99924 standard; Protein; 380 AA.
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11; Conservative
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/note= "Mature OCIF-CBst"
Misc_difference 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Signal peptide"
                                                331 irflhsftmyk 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  irflhsftmyk 358
                                                                                             IRFLHSFIMYK 12
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Matches
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 80. Page 126-128; 183pp. Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents a mutated version of the invention. This sequence represents to which Gln 371 is substituted by Leu and amino acids 373-380 of the mature OCIF protein are deleted. These changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore an analyse of the control of disorders of bone resorption, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No. According osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 62. Page 117-119; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CL in which amino acids 379-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1997 (first entry)
Mutated OCIF, OCIF-CL.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                       Score 94; DB 20; Length 393;
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94; DB 20; Length 399;
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-1995; JP-054977.
21-JUL-1995; JP-054977.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagwa M, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
N-PSDB; T33172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .T 10
R99942 standard; Protein; 399 AA.
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                   369 irflhsftmyk 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 irflhsftmyk 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IRFLHSFTMYK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-1996; J00374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IRFLHSFIMYK 12
                                                                                                                                                                                                                                                                                                                   393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis.
Synthetic.
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                                                                                                                                                                                                                                                                                                 osteoporosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R99942:
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C22S in which the 27nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 degr. Ocif is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1997 (first entry)
Mutated OCIF, OCIF.20S.
Osteoclastrogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                       22-APR-1997 (first entry)
Mutated OCIF, OCIF-C22S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 94; DB 20; Length 401; Pred. No. 5.77e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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20-FEB-1996; JP-054977.
21-JUL-1995; JP-207508.
(SNOW BRAND MIKK PROD CO LTD.
GCO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 12
R99932 standard; Protein; 401 AA.
                      T 11
R99934 standard; Protein; 401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein 22.401
/note= "Mature OCIF-C208"
                                                                                                                          /note= "Signal peptide"
Protein 22.401
/note= "Mature OCIF-C225"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1996.
20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc_difference 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 IRFLHSFTMYK 12
                                                                                                                                                            Misc_difference 277
                                                                                                                                                                                                                                                                                                                                                                                                                                             401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= C20S
W09626217-A1.
                                                                                                                                                                                 WO9626217-A1.
29-AUG-1996.
                                                                                                                                                                        /label= C22S
                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                               Synthetic.
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                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R99932;
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                      RESULT
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NA encoding osteoclastogenesis inhibitory factor protein - useful protein control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis Claim 41: Page 103-105; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCTF) of the invention. This captence represents OCTF-C23S in which the 23rd Cys residue in the mature OCTF protein is substituted by Ser. The OCTF of the invention of has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins of at 70 deg. C. or 30 mins at 56 deg.C. and is lost after 10 mins at 90 deg.C. OCTF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                                                                                                                                                                                   This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents oCIF-C20S in which the 20th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutated OCIF, OCIF-C23S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                   DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 32; Page 96-98; 183pp; Japanese.
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Morinaga T;
Yasuda H;
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Yasuda H;
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Pred. No. 5.77e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 94; DB 20; Length 401.
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-1996; J00374.
20-FEB-1996; JP-054977.
21-JUL-1995; JP-207508.
(SNOW DEAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shina N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
Kobayashi F, Mochizuki S,
Tsuda E, Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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R99935;
22-APR-1997 (first_entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative
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Local Similarity 100.0%;
les 11; Conservative
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/note= "Mature OCIF-C23S"
Misc_difference 400
/label= 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Signal peptide"
   Goto M, Higashio K,
Nakagawa N, Shima N,
WPI; 96-402320/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IRFLHSFTMYK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 AA;
                                                                                            N-PSDB; T33162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis
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Matches
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27 PCFEB-1996; JP-054977.

28 20-FEB-1996; JP-054977.

R 210-FEB-1995; JP-054977.

R 210-FIGH-1995; JP-054977.

R 210-FIGH-1995; JP-054977.

R 210-FIGH-1995; JP-057080.

R 210-FIGH-1995; JP-057080.

R 210-FIGH-1995; JP-057080.

R 210-FIGH-1995; JP-0508

R 210-FIGH-1996; JR-0508

                                                                                                                                                                                                                                                                                                         22-AFR-1997 (first entry)
Mutated OCIF, OCIF-C19S.
Osteqclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
osteoporosis.
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Pred. No. 5.77e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                      .r 114
R99931 standard; Protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R9992$ standard; Protein; 401 AA.
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22-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Mature OCIF-C19s" /isc_difference 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..21
"Signal peptide"
369 irflhsftmyk 379
                                         2 IRFLHSFTMYK 12
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W09626217-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
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TO R9
TO AC R9
DD 229
DD 529
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C
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Location/Qualifiers

Homo sapiens.

Peptide

/note|

Protein 22..401 /note= "Mature OCIF, claim 6"

6217-A1.

/note= W09626

29-AUG-1996

29-AUG-1996. 20-FEB-1996; JOO374. 20-FEB-1995; JP-054977.

"Signal peptide"

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ö
                                                                                                            DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone rescrition control, esp. treatment of osteoporosis Disclosure; Pege 64-66; 183pp; Japanese.

This sequence represents the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or useful in the control of bone rescription and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                               Morinaga T;
                                                               Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                           Score 94; DB 20; Length 401;
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: Tue Dec 2 14:46:45 1997
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:46:05 1997; MasPar time 2.71 Seconds 128.122 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-3 (1-12) from US08915004.pep 94 1 XIRFLHSFTMYK 12

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

91006 seqs, 28888923 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:annl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev Database:

Mean 25.879; Variance 44.392; scale 0.583 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ult No.	Score	Query Match	Query Match Length	DB		Description	Pred. No
	59	62.8	1441	4	: -	M polyprotein precur	6.93e+00
2	58	61.7	67	œ	F42525	A-ORF-S protein - va	9.85e+00
m	56	59.6	446	8	534570	beta-glucosidase (EC	1.97e+01
4	56	59.6	to			33	1.97e+01
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7	55	58.5	m	٦	S63652	hypothetical protein	•
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10	54	57.4	-		UYPVAD	О	٠
11	54	57.4	**		S09851	hypothetical protein	3.89e+01
12	53	56.4	3		B36841	C20L protein - vario	7.
13	53	56.4	ന		C42508	F16L protein - vacci	4
14	53	56.4	ന		S04349	nitrate reductase (N	4.
15	53	56.4	ന			nitrite reductase ni	5.42e+01
16	53	56.4	22	Н		sodium channel prote	•
17	53	56.4	\vdash	Н	A49132	faf-fat facets gene	5.42e+01
18	53	56.4	74	٦	B49132	faf=fat facets gene	5.42e+01
19	52	55.3	ഗ	П	543482		7.52e+01
20	52	55.3	m		S47846	rfaY protein - Esche	7.52e+01
21	52	55.3	m		A42981	RfaY - Escherichia c	7.52e+01

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ALIGNMENTS

TUT 1 RY RY My polyprotein precursor - La Crosse virus (isolate 74-32813) RAINS Glycoprotein G1; glycoprotein G2; nonstructural protein NS-M RAISM ANISM # (formal_name La Crosse virus 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 05-Jan-1996 A2937 A2937 A2937 A2937 # fittle # fittle # cross of the M RNA of an isolate of La Crosse virus. # fittle # cross_references MUID:88089508 # # accession # # molecule_type mRNA # # molecule_t	Gly Specific enzymatic cleavages in vivo yield mature proteins including nonstructural protein NS-M, glycoprotein Gl, and glycoprotein G2. However, exact cleavage sites are undetermined.	on segment M ** ** ** ** ** ** ** ** ** ** ** ** **	, #leng	Similarity 55.6%; Score 59; DB 4; Length 1441; Similarity 55.6%; Pred. No. 6.93e+00; 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	rflniyamy 396 ::: RFLHSFTM1 11	F42525 #type complete A-ORF-S protein • vaccinia virus (strains WR and Copenhagen)
RESULT 1 INTIE CONTAINS CONTAINS ORGANISM DATE ACCESSIONS # authors # journal # title # cross-referen # accession	Sp	GENETICS #map_position CLASSIFICATION KEYWORDS FEATURE 1-13 1-441	30,57,245,490, 1177 SUMMARY	Query Match Best Local S Matches	Db 388 rflr : Qy 3 RFLE	RESULT 2 ENTRY TITLE

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#type complete
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J. Gen. Virol. (1991) 72:1349-1376
Nucleotide sequence of 42kbp of vaccinia virus strain WR from
near the right inverted terminal repeat.
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submitted to the EMBL Data Library, July 1993
Comparative amino acid sequence analysis of Thermotoga
maritima Beta-glucosidase BglA deduced from the nucleotide
sequence of its gene indicates distant relationship between
family BGA Beta-glucosidases and other families of Beta-1
4-glycosyl hydrolases.
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Mol. Gen. Genet. (1994) 242:111-115
Comparative amino acid sequence analysis of Thermotoga
maritima beta-glucosidase (BglA) deduced from the
nucleotide sequence of the gene indicates distant
relationship between beta-glucosidases of the BGA family
and other families of beta-1,4-glycosyl hydrolases.
                                 host Homo sapiens (man)
09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change
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Pred. No. 9.85e+00;
3; Mismatches 2; Indels
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Pred. No. 1.97e+01;
2; Mismatches 3; Indels
                                                                                                                     Johnson, G.P. submitted to GenBank, June 1990
                    #formal_name vaccinia virus
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##cross-references EMBL:X74163
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JQ1767
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Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoefte, H.; Soetaert, P.; Jansens, S.; Peferoen, M. Nucleic Acids Res. (1990) 18:5545
Nucleotide sequence and deduced amino acid sequence of a new Lepidoptera-specific crystal protein gene from Bacillus
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parasporal crystal protein - Bacillus thuringiensis
#formal_name Bacillus thuringiensis
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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hypothetical protein M70711 - Methanococcus jannaschii
#formal_name Methanococcus jannaschii
13.Sep-1996 #sequence_revision 13-Sep-1996 #text_change
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#length 1160 #molecular-weight 130968 #checksum 7196
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3; Mismatches 1; Indels
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Best Local Similarity 60.0%; Pred. No. 1.97e+01
Matches 6; Conservative 3; Mismatches
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187-211
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Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C. Science (1996) 273:1058-1073

Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein 785 - Allomyces macrogynus mitochondrion #formal_name mitochondrion Allomyces macrogynus 28-oct-1996 #text_change
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J. Mol. Biol. (1996) 255:688-701
The mitochondrial DNA of Allomyces macrogynus: the complete genomic sequence from an encestral fungus.
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Biochem. Biophys. Res. Commun. (1993) 195:866-873
Molecular cloning of a novel human melanocortin receptor.
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#formal_name Homo sapiens #common_name man
14-Jul-1994 #sequence_revision 14-Jul-1994 *text_change
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##residues 1-785 ##label PAO
##cross-references EMBL:U41288
XY #length 785 #molecular-weight 88119 #checksum 2052
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                                                                                                                                                                                            preliminary; nucleic acid sequence not shown;
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##cross-references GB:L77117; TIGR:MJ0711; CDS_PID:g1510799
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#length 322 #molecular-weight 38631
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Pred. No. 2.77e+01;
3; Mismatches 1;
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##cross-references EMBL:225470
##experimental_source brain
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Best Local Similarity 55.6%;
atches 5; Conservative
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UYPVAD #type complete noncapsid protein NSI - Aedes densovirus (strain GKV 002 002) #formal_name Aedes densovirus host Aedes aegypti (yellow fever mosquito) 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Apr-1994
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#journal Virology (1991) 185:323-336
#title Nucleotide sequence and genomic organization of Aedes
densonucleosis virus.
#cross-references MUID:92024690
#accession A40784
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#domain transmembrane #status predicted #label TMI\
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#domain transmembrane #status predicted #label TM5\
#binding_site carbohydrate (Asn) (covalent) #status predicted #label TM7\
#Pinding_site carbohydrate (Asn) (covalent) #status #length 325 #molecular-weight 36618 #checksum 589
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5R protein - human herpesvirus 6 (strain Uganda-1102)
#formal_name human herpesvirus 6
26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change
08-Apr-1994
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Lawrence, G.L.; Chee, M.; Craxton, M.A.; Gompels, U.A.;
Honess, R.W.; Barrell, B.G.
J. Virol. (1990) 64:287-299
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(Y #length 772 #molecular-weight 88746 #checksum 7872
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#length 849 #molecular-weight 97542 #checksum 1776
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ICATION **superfamily Aedes densovirus noncapsid protein NS1
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Pred. No. 3.89e+01;
0; Mismatches 1; Indels
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Best Local Similarity 55.6%; Pred. No. 3.89e+01;
Matches 5; Conservative 1; Mismatches 3; Indels
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##molecule_type DNA
##molecule_type 1-849 ##label AFA
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Matches 6; Conservative
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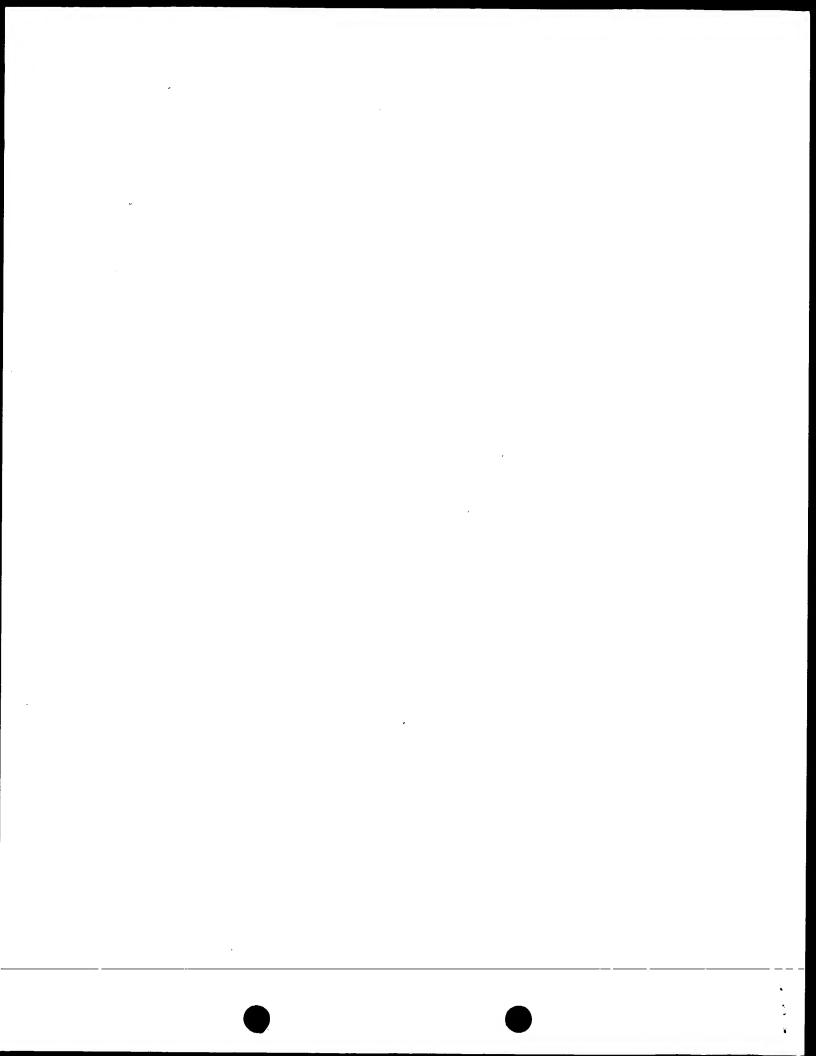
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#title Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.
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hypothetical protein UL87 - human cytomegalovirus (strain
                                 Gaps
                                                                                                                                                                                                         #formal_name human cytomegalovirus, human herpesvirus 5
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07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
27-Jan-1995
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#formal_name variola virus
30.Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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.X #length 231 #molecular-weight 26497 #checksum 4488
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               Best Local Similarity 30.0%;
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Best Local Similarity 50.0%;
Matches 5; Conservative
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Fauthors
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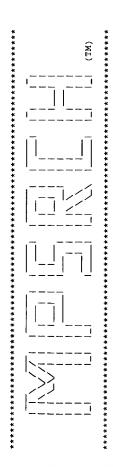
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Bell, A.I.; Gaston, K.L.; Cole, J.A.; Busby, S.J.W.
#journal Nucleic Acids Res. (1989) 17:3865-3874
#title Cloning of binding sequences for the Escherichia coli
transcription activators, FNR and CRP: location of bases
involved in discrimination between FNR and CRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             S04349  #type complete
nitrate reductase (NADH) (EC 1.6.6.1) - Escherichia coli
#formal_name Escherichia coli
15-0ct-1994 #sequence_revision 15-0ct-1994 #text_change
                                  host Homo sapiens (man)
09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change
                                                                                                                                                                                                                                                                                                                     Gaps
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nitrite reductase nirB - Escherichia coli
#formal_name Escherichia coli
21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
10-Nov-1995
                                                                                                                                                                                                                                          #length 231 #molecular-weight 26605 #checksum 7005
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#length 838 #molecular-weight 92717 #checksum 1768
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F16L protein - vaccinia virus (strain Copenhagen)
#formal_name vaccinia virus
                                                                                                                                                                                                                                                                          Score 53; DB 8; Length 231;
Pred. No. 5.42e+01;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 9; Length C. Score 53; DB 9; Length C. S. 42e+01;
                                                                                                                              Johnson, G.P. submitted to GenBank, June 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation not shown
                                                                                                                                                                                                                       1-231 ##label JOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-838 ##label BEL
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                                                                                                                                                                                    preliminary
                                                                                                                                                                                                                                                                              / Match 56.4%;
Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 56.4%;
Local Similarity 40.0%;
nes 4; Conservative
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                                                                        08-Apr-1994
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                       ##molecule_type DNA
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                                                                                                                              #authors
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                                                                                            ACCESSIONS
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                                                                                                                                                                                                                                                                                                               Matches
                                                                                                             REFERENCE
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##molecule_type DNA
##residues 1-839 ##label PEA
GENETICS
#gene nirB
SUMMARY

Query Match 56.4%; Score 53; DB 9; Length 839;
Best Local Similarity 40.0%; Pred. No. 5.42e+01;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps. 0;
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Db 730 ikyldrfmmf 739 |::| | |: Qy 2 IRFLHSFTMY 11 Search completed: Tue Dec 2 14:46:16 1997 Job time: 11 secs.





Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:45:38 1997; MasPar time 1.94 Seconds 130.901 Million cell updates/sec Run on:

pular output not generated.

>US-08-915-004-3 (1-12) from US08915004.pep 94 Title: Description: Perfect Score:

1 XIRFLHSFTMYK 12 Sequence: PAM 150 Gap 15 Scoring table:

Post-processing:

59021 segs, 21210388 residues

Searched:

Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 26.933; Variance 36.903; scale 0.730 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	0	% Query	% Query Match Ionath	2	Ę.	,	7000
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]	59	62.8	1441	10	VGLM_BUNL7	M POLYPROTEIN PRECURS	1.41e+00
7	58	61.7	67	디	YVAS_VACCV	HYPOTHETICAL 7.5 KD P	2.14e+00
m	58	61.7	790	11	YP84_CAEEL	HYPOTHETICAL 90.9 KD	2.14e+00
4		9.09	174	11	YRKL_BACSU	HYPOTHETICAL NAD(P)H	3.26e+00
ហ		59.6		-	BGLA_THEMA	BETA-GLUCOSIDASE A (E	4.92e+00
9	26	59.6		7	CRYS_BACTA	132 KD CRYSTAL PROTEI	4.92e+00
7	54	57.4		9	MC5R_HUMAN	MELANOCORTIN-5 RECEPT	1.10e+01
∞	54	57.4		10	UL87_HSV6U	PROTEIN US8.	1.10e+01
თ	54	57.4		10	UL87_HSV7J	PROTEIN U58.	1.10e+01
10	54	57.4		10	VNCS_AEDEV	NONCAPSID PROTEIN NS-	1.10e+01
11	54	57.4		10	UL87_HCMVA	PROTEIN UL87.	1.10e+01
12	53	56.4	231	10	VF16_VARV	PROTEIN F16.	1.64e+01
13	23	56.4	231	10	VF16_VACCP	PROTEIN F16.	1.64e+01
14	53	56.4		10	VF16_VACCC	PROTEIN F16.	1.64e+01
15	53	56.4		11	YDC8_SCHPO	HYPOTHETICAL 84.0 KD	1.64e+01
16		56.4	847	9	NIRB_ECOLI	NITRITE REDUCTASE (NA	1.64e+01
17	23	56.4		~	CIN1_LOLBL	SODIUM CHANNEL PROTEI	1.64e+01
18	52	55.3		œ	RECX_PSEFL	REGULATORY PROTEIN RE	2.42e+01
19	52	55.3	~	œ	RFAY_ECOLI	LIPOPOLYSACCHARIDE CO	2.42e+01
20		55.3		11	YD3B_SCHPO	HYPOTHETICAL 33.1 KD	2.42e+01
21	52	55.3	330	œ	QUTG_EMENI	QUIG PROTEIN.	2.42e+01
22	52	55.3	468	11	YL34_CAEEL	HYPOTHETICAL 53.6 KD	2.42e+01

22.22.24.44.44.44.44.44.44.44.44.44.44.4
GLUCOSYLCERAMIDASE PR HYPOTHETICAL ZINC MET ATP SYNTHASE ALPHA CH PUTATIVE RNA HELICASE PUTATIVE RNA HELICASE PUTATIVE RNA HELICASE PUTATIVE RNA HELICASE ARYLPHORIN ALPHA SUBU DNA-DIRECTED RNA POLY RNA POLYMERASE BETA S FLAVONOL 3-SULFOTRANS HYPOTHETICAL 40.9 KD CONGLUTININ PRECURSOR GAG POLYPROTEIN (CONT THREONYL-TRNA SYNTHET 70 KD PEROXISOMAL MEM 71 KHANSPORASE FOR TRANS THANSPORASE FOR TRANS THANSPORASE FOR TRANS
GLCM_MOUSE YVD3_CAEEL ATPA_METBA VIOB_VACY VIOB_VACC ARYA_MANS RPOM_TEAST RPOM_TEAST RPOM_TEAST RPOM_TEAST RPOM_TEAST RPOM_TEAST RRPL_COVO B3ST_ELACH CONG_BOVIN GAG_BAEVM RPOM_THOAN BMP7_HOMAN PMP7_RAT ARYB_MANSE MEPA_MOUSE HSS1_RAT TRAA_ECCULT TSCC_PSEAM
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## ALIGNMENTS

Score 59; DB 10; Length 1441; Pred. No. 1.41e+00; 62.8%; 55.6%; Query Match Best Local Similarity ö

Gaps

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ALIEBL W., GABELGEBERGER J., SCHLEIFER K.H.;

LIEBL W., GABELGEBERGER J., SCHLEIFER K.H.;

MOL. GEN. GENET. 242:111-115(1994).

-! CATALTIC ACTIVITY: HYDROLYZIS OF TERMINAL, NON-REDUCING BETA-D-GLUCOSE RESIDUES WITH RELEASE OF BETA-D-GLUCOSE.

-!- PATHWAY: CELLULOSE DEGRADATION.

-!- SHIMARARY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.

RMB1, X74168; G395291; --

--- SHILABRIY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.

RMB1, X741661.

RPR: 334570: S34570.

RPR: S41561: S41561.

RPR: SA1561: S41561.

RPR: SA1561: S41561.

RPR: SA1561: S41561.

RPR: SA1561: SA1561.

RPR:                                                                                                                                                                                                                                              01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOPATION UPDATE)
HYPOTHETICAL NAD(P)H OXIDOREDUCTASE IN BLITR-SPOILIC INTERCENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                       PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-168 / JH642;
KOBAZASHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO S.,
SATO T., TAKEUCHI M.,
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: STRONG, TO E.COLI YABF, YHER AND H.INFLUENZAE HI1544.
-!- SIMILARITY: STRONG, TO MAWMALIAN NAD(P)H DEHYDROGENASE (QUINONE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1994 (REL. 30, CREATED)
01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
BETA-GLUCOSIDASE A (RC 3.2.1.21) (GENTIOBIASE) (CELLOBIASE) (BETA-D-GLUCOSIDE GLUCOHYDROLASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57; DB 11; Length 174 Pred. No. 3.26e+00; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 59.6%; Score 56; DB 1; Length 446; Best Local Similarity 50.0%; Pred. No. 4.92e+00;
                                         Indels
Best Local Similarity 50.0%; Pred. No. 2.14e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D84422; G1303711; -.
SUBILLIST; BG11778; YRKL.
HYPOTHETICAL PROTEIN; OXIDOREDUCTASE.
SEQUENCE 174 AA; 20093 MW; AD4DECD8 CRC32;
                                                                                                                                                                                                         174 AA.
                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROKARYOTA; NOT YET CLASSIFIED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.6%;
Best Local Similarity 60.0%;
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                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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STRAIN-MSB8 / DSM 3109;
MEDLINE; 94104595.
                                                                                303 ikfilafsmy 312
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2 IRFLHSFIMY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 IRFLHSFTMY 11
                                                                                                                                                                                                                                                                                                                                                     BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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BGLA_THEMA
Q08638;
                                                                                                                                                                                                    YRKL_BACSU
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                   Gaps
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VENCIMIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).
VIRLÍDAE: DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
ORTHÓPOXVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAİN=COPENHAGEN;
MEDLİNE; 91021027.
GÖRBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-COPENHAGEN;
GOBBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB 11; Length 67; Pred. No. 2.14e+00; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 67;
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL 90.9 KD PROTEIN CO8BIL.4 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMMS M.;
SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED 146676; G576997; --
WORNPEP; C08B11.4; CE01474.
HYPOTHETICAL PROTEIN.
SEQUENCE 790 AA; 90873 MW; 8B2A0D83 CRC32;
                   ;
;
                                                                                                                                                                                                                      01-FB-1991 (REL. 17, CREATED)
01-FBB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-GCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
HYPOTHEFICAL 7.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PACLETIE:
VIROLOGY 179:517-563(1990).
EMBL; M35027: 633522; -
PIR; 445525; F42525.
PIR; JQ1824; JQ1824.
HYPOTHETICAL PROTEIN.
SEQUENCE 67 AA: 7503 MW; 7884D470 CRC32;
                   3; Mismatches
                                                                                                                                                                                 67 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     790 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMITH G.L., CHAN Y.S., HOWARD S.T.;
J. GEN. VIROL. 72:1349-1376(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAOLETTI E.;
VIROLIOGY 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.7%;
Best Local Similarity 50.0%;
Matches 5; Conservative
                   5; Conservative
                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                        388 rflniyamy 396
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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IRFLHSFTMY 11
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                                                                                  3 RFLHSFTMY 11
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MEDLINE; 91259063.
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HOLLEIC ACIDS RES. 18:5545-5545[1990].
- I- FUNCTION: PROMOTES COLLOIDOSONOTIC LYSIS BY BINDING TO THE MIDGUT
- PUNCTION: PROMOTES COLLOIDOSONOTIC LYSIS BY BINDING TO THE MIDGUT
- PUTLELLAL CELLS OF MANY LEPHDOPPERAN LARVAE.
- TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
- I- TOXIC SEGMENT OF THE PROTEIN IS PRODUCED DURING.
- POPULANTION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACILLUS THURINGIENSIS (SUBSP. AIZAWAI).
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
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   Gaps
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01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
132 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRIFFON N., MIGNON V., FACCHINETTI P., DIAZ J., SCHWARTZ J.C.,
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Pred. No. 4.92e+00;
3; Mismatches 1; Indels
   Indels
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CHHAJLANI V., MUCENIECE R., WIKBERG J.E.S.;
BIOCHEM. BIOPHYS. RES. COMMUN. 195:866-873(1993).
3;
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
MELANOCORTIN-5 RECEPTOR (MC5-R) (MC-2).
   Mismatches
                                                                                                                                                                                                                                                                            PRT; 1165 AA.
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Similarity 60.0%;
6; Conservative
5; Conservative
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                                                                    239 vrfmhqfnny 248
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                                                                                                               2 IRFLHSFIMY 11
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MEDLINE; 91016842.
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2 IRFLHSFTMY 11
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MEDLINE; 95258173.
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P33032;
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FATHI Z., IBEN L.G., PARKER E.M.;
NEUROCHEM. RES. 20:107-113(1994).
-!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
ADENYIANTE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
IMMUNOMODULATION PROPERTIES OF MELANOCORTINS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: IS EXPRESSED IN THE BRAIN BUT NOT IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U58 OR 5R.
HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                     MELANOMA CELLS.
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; 225470; 6397610; --
EMBL; 127080; 6435600; --
GRAB; GCR_09353; 6522164; --
GCRDB; GCR_0793; --
GCRDB; GCR_0793; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
POTENTIAL.
PALMITATE (POTENTIAL).
PALMITATE (POTENTIAL).
R -> A (IN REF. 2).
ALPGASSARQHISM -> LCPGPALRGRGPAW (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 90080132.
LAWRENCE G.L., CHEE M., CRAXTON M.A., GOMPELS U.A., HONESS R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54; DB 6; Length 325;
Pred. No. 1.10e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                          G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.

DOMAIN 137 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                     1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULA: (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REF. 1).
F -> Y (IN REF. 2)
237C436E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    772 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                   MIM; 600042; -.
PROSITE; PS00237; G_PROTEIN_RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, LAST SEQU
01-OCT-1996 (REL. 34, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36600 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. VIROL. 64:287-299(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.4%;
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     22459
22439
22439
22439
22439
22439
22439
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SEQUENCE FROM N.A. STRAIN-BANGLADESH-1975;
                                                                                                                      LT 11
UL87_HCMVA
P16730;
                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                      RESULT
                                                              g
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                                                                                                                                                        Gaps
      MARTÍN M.E., EFSTATHIOU S., CRAXTON M., MACAULAY H.A.;
VIROÚGOY 209-20-51 (1995).

1. SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER EBV BCRFI,
HSV-6 U58, HVS-1 24 AND HCMV UL87.

EMBL., M68963; G325501; -.
BTRL., R33413; G854037; -.
PIR. F33560; F33560.

SEQUENCE 772 AA; 88746 MW; 9AD5BCIF CRC32;
                                                                                                                                                                                                                                                                                                                                  HERPES SIMPLEX VIRUS (TYPE 7 / STRAIN JI) (HHV7).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                           NICHOLAS J.;
SUBMIGTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER EBV BCRF1,
HSV-6 U58, HVS.1 24 AND HCMV UL87.
EMBL, U43400; G1139661; C0C9D789 CRC32;
SEQUENCE 775 AA; 89413 MW; C0C9D789 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEDES DENSONUCLEOSIS VIRUS (STRAIN GKV 002 002) (AEDES DENSOVIRUS).
VIRIDAE: SS-DNA NONENVELOPED VIRUSES; PARVOVIRIDAE; DENSOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE: 9202409.

AFANASIEV B.N., GALYOV E.E., BUCHATSKY L.P., KOZLOV Y.V.;

AFANASIEV B.N., GALYOV E.E., BUCHATSKY L.P., KOZLOV Y.V.;

VIROLGOY 185:323-336 (1991).

-!- FUNCTION: SEEMS NECESSARY FOR VIRAL DNA REPLICATION, PLAYS AN IMPORTANT ROLE IN THE REGULATION OF CAPSID GENE EXPRESSION. IT IS COVALENTLY BOUND TO THE 5'TERMINI OF VIRAL DNA, AND CAN IMPLENCE DNA PACKAGING. NSI IS ALSO BELIEVED TO POSSESS THE TOPOLSOMERASE I TYPE NICKING ACTIVITY, AND CYTOTOXIC ACTIVITY.

EMBL: MA7899; -: NOT AND ANNOTATED_COS.

PIR: A40784: UTYPAD.
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01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NONCAPSID PROTEIN NS-1 (NONSTRUCTURAL PROTEIN NS1) (NCVP1).
                                                                                                                             Score 54; DB 10; Length 772;
Pred. No. 1.10e+01;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54; DB 10; Length 775;
Pred. No. 1.10e+01;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NONCAPSID PROTEIN; DNA REPLICATION; ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
; FFC7C288 CRC32;
                                                                                                                                                                                                                                                                      01-0¢T-1996 (REL. 34, CREATED)
01-0¢T-1996 (REL. 34, LAST SEQUENCE UPDATE)
10-0¢T-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTEIN US8
                                                                                                                                                                                                                                                   775 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    849 AA.
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                                                                                                                             Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                  STANDARD;
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MEDLINE; 95266321
                                                                                                                                                                              470 hsfvmyk 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hsfvmyk 467
                                                                                                                                                                                                   6 HSFTMYK 12
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                                                                                                                                                                                                                                                UL87 HSV7J
P52363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ULT 10
VNCS_AEDEV
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SEQUENCE
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                                                                                                                                                                                                                                                                                                HUMAN CYTOMEGALOVIRUS (STRAIN AD169).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE; ORTHOPOXVIRUSES.
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STRAIN-INDIA-1967 / ISOLATE IND3;
MEDLINE; 94152154.
SHCHELKUNOV S.N., BLINOV V.M., RESENCHUK S.M., TOTMENIN A.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 10; Length 941;
Pred. No. 1.10e+01;
0; Mismatches 1; Indels
       Length 849;
                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-INDIA-1967 / ISOLATE IND3;
MEDLINE; 93202281.
SHCHEKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;
FEBS LETT. 319:80-83(1993).
     Score 54; DB 10;
Pred. No. 1.10e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                591 591 POTENTIAL.
661 661 POTENTIAL.
801 801 POTENTIAL.
941 AA: 104803 MW; A9C56CC3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SULT 12
VF16_VARV STANDARD; PRT; 231 AA. P33874; O1-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PROTEIN F16.
F16L OR C20L.
VARIOLA VIRUS.
                                                                                                                                                                                                            01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                          Mismatches
                                                                                                                                                                                 941 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                 PRT;
Best Local Similarity 30.0%;
Matches 3: Concerning 30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.4%;
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SANDAKHCHIEV L.S.;
VIRUS RES. 30:239-258(1993)
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37
591
661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S09851; S09851.
                                                                       416 vkflrnyily 425
                                                                                                          2 IRFLHSFTMY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 hsfvmyk 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 HSFTMYK 12
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EMBL; M35027; G335383; -. PIR; C42508; C42508.
SEQUENCE 231 AA; 26605 MW; C59DF26C CRC32;
                                                                                                                                                                                                                                                                                                                                   ESULT 13

VELGACCE STANDARD; PRT; 231 AA.

PV16492;
TO1-APR-1993 (REL. 25, CREATED)
TO1-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
TO1-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
TO1-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
TO1-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
TO1-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
S VACCINITA VIRUS (STRAIN L-IVP).
C VIRIDAE: DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILIDE, 91021027.
GOEBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.
PAOLETII E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VACCINIA VIRUS (STRAIN COPENHAGEN).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MIRRYUKOV N.N., CHIZHIKOV V.E., PRIKHOD'KO G.G., URAMANOV I.M.,
SERPINSKII O.I., BLINOV V.M., NIKULIN A.E., VASILENKO S.K.;
BIOTEKHNOLGSIYA 4:442-449(1988).
EMBL; M57977; G335696; --
            MASSUNG R.F., ESPOSITO J.J., LIU L., QI J., UTTERBACK T.R., KNIGHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N., SELIVANOV N.A., CAVALLARO K.F., KERLAVAGE A.R., MAHY B.W.J., VENTER C.J., NATURE 366:748-751(1993).

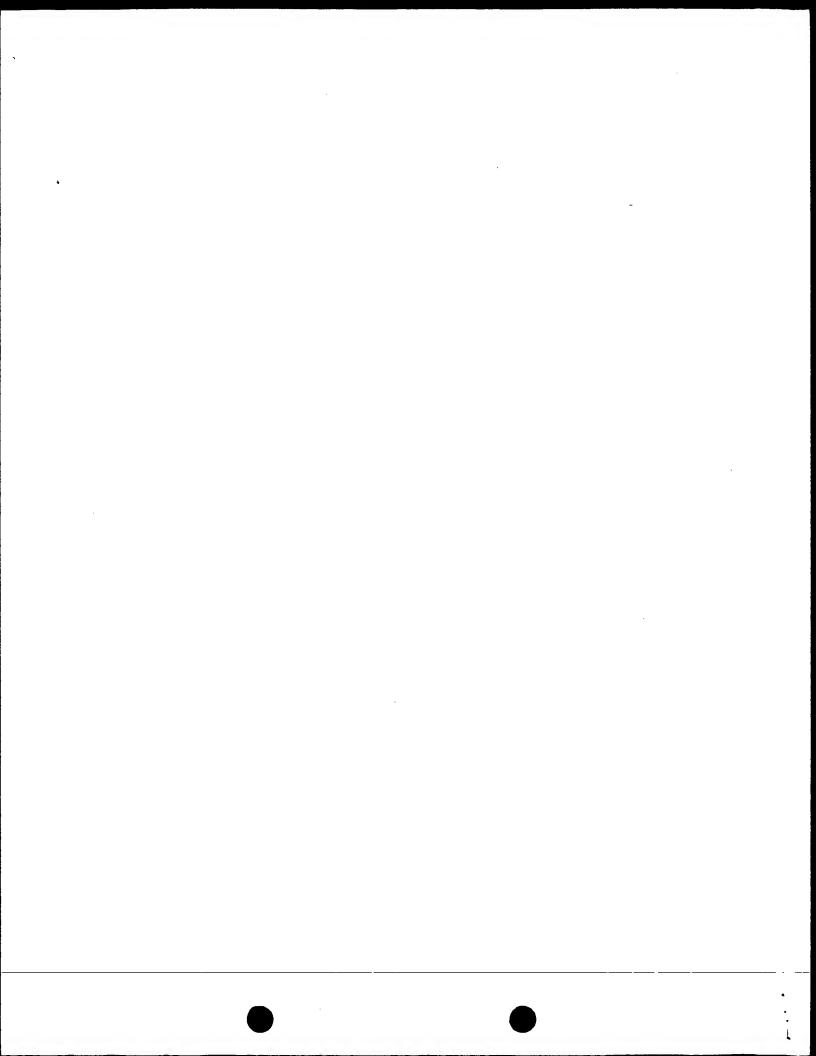
EMBL: X69198; G297221; ---
EMBL: X69198; G297221; ---
EMBL: L25579; G438958; ---
PIK; B36841; B36841; B36841.

SEQUENCE 231 AA; 26497 MW; 096C212B CRC32;
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                                                                                                                                                                                   Score 53; DB 10; Length 231;
Pred. No. 1.64e+01;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 56.4%; Score 53; DB 10; Length 231; Best Local Similarity 50.0%; Pred. No. 1.64e+01; Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26550 MW; 32D97918 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                     Query Match
Best Local Similarity 50.0%;
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                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 rfvnklkmyk 207
                                                                                                                                                                                                                                                      198 rfvnklkmyk 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RFLHSFTMYK 12
                                                                                                                                                                                                                                                                         3 RFLHSFTMYK 12
MEDLINE; 94088747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORTHOPOXVIRUSES.
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P21021;
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RX
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                                    Gaps
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--- SIMILARITY: STRONG, TO YEAST PRT1/CDC63.

EMBL; Z70691; E234481; --
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             watch 56.4%; Score 53; DB 11; Length 725; Local Similarity 44.4%; Pred. No. 1.64e+01; es 4; Conservative 4; Mismatches 1; Indels
 Length 231
Score 53; DB 10; Length 231
Pred. No. 1.64e+01;
3; Mismatches 2; Indels
                                                                                                                                                                                  OL-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
HYPOTHETICAL 84.0 KD PROTEIN C25G10.08 IN CHROMOSOME I.
SPAC25G10.08
SCHIZOSACCHAROMYCES POWBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                             725 AA; 84035 MW; 56EA1958 CRC32;
                                                                                                                                                          725 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: Tue Dec 2 14:45:47 1997 Job time : 9 secs.
Query Match 56.4%;
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                          STANDARD;
                                                              198 rfvnklkmyk 207
                                                                                | | | : : | | | | 3 RFLHSFTMYK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 rflhpyvkf 237
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RFLHSFTMY 11
                                                                                                                                        LT 15
YDC8_SCHPO
Q10425;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Dec 2 14:50:15 1997; MasPar time 8.93 Seconds 523.035 Million cell updates/sec Run on:

alar output not generated.

rtle:

Description: Perfect Score: Sequence:

>US-08-915-004-4
(1-380) from US08915004.pep
286.1
ETFPPKYLHYDEETSHQLLC.......QKLFLEMIGNQVQSVKISCL 380

PAM 150 Gap 11 Scoring table:

101610 seqs, 12294212 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq28
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 Database:

Mean 34.473; Variance 144.575; scale 0.238 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Pred. No.	2.03e-275	2.03e-275	5.51e-274	5.51e-274	1.42e-273	2.87e-273	2.27e-273	7	1.48e-268	1.89e-242	N	1.63e-236	5.85e-211	1.25e-209	1.60e-199	1.94e-195	7	-17	2e-1	2.53e-123	
	lastogen	steoclas	OCIF-C1	OCIF-C2	OCIF-C2	OCIF-CL	OCIF-C2	OCIF-C2	OCIF-CB	OCIE-DC	necrosis	OCIF-CC	OCIF-CS	OCIF-DC	OCIF-DC	OCIF-DC	OCIF-DD	OCIF-CD	OCIE-DD	OCIF-CD	
Description	Mature osteoclastogen	Full length osteoclas	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Human tumour	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	Mutated OCIF,	
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DB	20	20	20	20	20	20	20	20	20	20	50	20	20	20	20	20	20	20	20	20	
% Query Match Length	380	401	401	401	401	399	401	401	393	360	390	351	321	359	360	359	327	272	326	197	
% Query Match	100.0	100.0	99.5		99.4	99.3	99.3	99.0	7.76	88.7	88.7	86.7	78.0	77.5	74.1	72.7	67.1	6.99	54.5	47.9	
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## ALIGNMENTS

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actor. OCIF; heparin; bone resorption; Ochizuki S, Morinaga T; d, Yano K, Yasuda H;	N-PSDB; 136685.  N-PSDB; 136685.  DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis for bone resorption control, sp. dayersents the mature osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. Sequence 380 AA;		etfppkylhydeetshqllcdkcppgtylkghctakwktvcapcpdhyytdswhtsdecl 	ysspyckelgyvkgecnrthnryceckegryleiefolkhrsoppgfgyvgagtpernty 
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R99924 standard; Protein; 380 AA. R99924; 22-APR-1997 (first entry) Mature osteoclastogenesis inhibitory factor osteoprossis. Homo sapiens. Homo sapiens. 29-AUG-1996; 20-FEB-1996; 20-FEB-1996; 21-JUL-1995; JP-054977. 21-JUL-1995; JP-054977. CGCO M. Higashio K. Kobayashi F. Goto M. Higashio K. Tsuda E. Ueda	WPF, 96-402320/ N-PSDB, T36685. NA encoding 136685. Claim 6; Page 6 Claim 6; Page 6 This sequence recorp factor (OCIF) o SDS-PAGE of 60 reducing condit or heparin and 30 mins at 56 d useful in the c treatment and p osteoporosis.	ch 1 s 38	tfp     TFP	CSP
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This sequence represents the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
ckrcpdgffsnetsskapcrkhtncsvfgllltqkgnathdnicsgnsestqkcgidvtl 180
                   ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrqhssqeqtfqllklwkhqn 240
                                                                                 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkygaediektikackp 300
                                                                                                                                              22-Apr-1997 (first entry)
Full length osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; oCIF; heparin; bone resorption;
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T; Nakagwa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H; NN-PSDB; 136685.
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Local Similarity 100.0%; Pred. No. 2.03e-275;
Nes 380; Conservative 0; Mismatches 0:
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                                                                                                                                                                                                                                                                                                                                                  standard; Protein; 401 AA.
                                                                                                                                                                                                                                                       gklflemigngvgsvkiscl 380
                                                                                                                                                                                                                                                                       Protein 22..401
/note⊨ "Mature OCIF, claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
/note⊨ "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                osteoporosis.
Homo sapiens.
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262 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkygaediektikackp 321
                                                                                                                                                            sdqilkllslwrikngdqdtlkglmhalkhsktyhfpktvtqslkktirflhsftmykly 381
                                                                                                                                                                                                                                                                                        22-APR-1997 (first entry)
Mutated OCIF, OCIF-019S.
OSteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morinaga T;
Yasuda H;
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Pred. No. 5.51e-274;
0; Mismatches 1; Indels 0;
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29-AUG-1996.

29-AUG-1996.

R 20-FEB-1995; JP-054977.

PR 21-JUL-1995; JP-207508.

PA (SNOW ) SNOW BRAND MILK PROD CO LTD.

GOLO M, Higashio K, Robayashi F, Mochizuki S, Morand M, Shimma N, Tsuda E, Ueda M, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano K, Yano
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1 Similarity 99.7%;
379; Conservative
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/note= "Mature OCIF-C195"
Misc_difference 195
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/note= "Signal peptide"
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Best Local Similarity
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoprosis claim 31. Page 96-98. 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C20S in which the 20th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption of disorders of bone resorption, e.g.
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                               121 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
                                                                                                 262 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkvgaediektikackp 321
                                                                                                                   22-APR-1997 (first entry)
Mutated OCIF, OCIF-C20S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
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Pred. No. 5.51e-274;
0; Mismatches 1; Indels 0;
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRRAND MILK PROD CO LTD.
GOCO M, HIGASHLO K, KODAYASHI F, MOCHIZUKI S,
MAKAGAWA N, Shima N, Tsuda E, Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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R99932 standard; Protein; 401 AA.
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Local Similarity 99.7%;
les 379; Conservative
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/note= "Signal peptide"
Protein 22..401
/note= "Mature OCIF-C20S"
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N-PSDB; T33162.
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                                                                                                                                                                                                                                                                                                                                                                                                                       osteoporosis.
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61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120

142 ckrcpdgffsnetsskapcrkhtncsvfgllltqkgnathdnicsgnsestqkcgidvtl 201

82 ycspvckelgyvkgecnrthnrvceckegryleiefclkhrscppgfgvvgagtperntv 141

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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 35; Page 98-100, 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C21S in which the 21st Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. Or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Mutated OCIF, OCIF-C21S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
                                                                                                              kdgdivkkiigdidlcensvgrhighanltfeqlrslmeslpgkkvgaediektikackp 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 etfppkylhydeetshqllcdkcppgtylkghctakwktvcapcpdhyytdswhttdecl 81
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                                               202 seeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrghssgegtfgllklwkhgn
                                                                Score 2843; DB 20; Length 401;
Pred. No. 1.42e-273;
2; Mismatches 1; Indels 0;
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20-FEB-1995; JP-205497.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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R99933 standard; Protein; 401
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Local Similarity 99.2%;
les 377; Conservative
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Protein 22..401
/note= "Mature OCIF-C21S"
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim [6.2] Page 117-119; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CL in which amino acids 379-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
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                   322 sdgilkllslwrikngdqdtlkglmhalkhsktyhfpktvtqslkktirflhtftmykly 381
                                                                                                                                                                                                                262 kagdivkkiigdidlsensvarhighanltfeglrslmeslpgkkygaediektikackp 321
                                                                                                                                                                                                                                                                                                                                                                                                                Mutated OCIF, OCIF-CL.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                  ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrghssgegtfgllklwkhgn
142 ckrcpdgffsnetsskapcrkhtncsvfgllltqkgnathdnicsgnsestqkcgidvtl
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20-FEB-1996.
20-FEB-1996.
21-UUL-1995; JP-207508.
21-UUL-1995; JP-207508.
3NOW BRAND MILK PROD CO LTD.
GOOD M. Higashio K. Kobayashi F. Mochizuki S.
Makagawa N. Shima N. Tsuda E. Ueda M. Yano K.
N-PSDB: T33172.
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0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                               R9994 2 standard; Protein; 399 AA.
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Best Local Similarity 100.0%;
Matches 378; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein 22..399 /note= "Mature OCIF-CL"
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Synthetic.
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 38: Page 100-102, 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C22s in which the 22nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SSS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchanges or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
sdqiiklislwrikngdqdtlkglmhalkhsktyhfpktvtqslkktirflhsftmykly 381
                                                                                 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKHQN 240
                                                                                                                    262 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkvgaediektikackp 321
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                                                                                                                                           241 KDQDIVKKIIQDIDLCENSVQRHIGHANLIFEQLRSLMESLPGKKVGAEDIEKTIKACKP
                                                   ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrghssgegtfgllklwkhgn
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Yasuda H;
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20-FEB-1996; J00374.
20-FEB-1995; JP-207508.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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1 Similarity 99.5%;
378; Conservative
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"Mature OCIF-C228"
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/label= C22S
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N-PSDB; T33164
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22-APR-1997
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202 ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrghssgegtfgllklwkhgn

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262 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkvgaediektikackp  යු

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osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C235 in which the 23rd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C. and ins at 56 deg. C, and is lost after 10 mins at 90 deg. C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
              262 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkygaediektikaskp 321
                                                                                                                                                                       sdqilnllslwrikngdqdtlkglmhalkhsktyhfpktvtqslkktirflhsftmykly 381
                                                                                                                                                                                                                                                                                                                                                                         Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding osteoclastogenesis inhibitory factor protein - useful
ckrcpdgffsnetsskapcrkhtncsvfgllltqkgnathdnicsgnsestqkcgidvtl
                                                       ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrqhssqeqtfqllklwkhqn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for bone resorption control, esp. treatment of osteoporosis
Claim 41; Page 103-105; 183pp; Japanese.
This sequence represents a mutated version of the full length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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R99935 standard; Protein; 401 AA.
                                                                                                                                                                                                                                           361 QKLFLEMIGNQVQSVKISCL 380
                                                                                                                                                                                                                             382 qklflemignqvqsvkiscl 401
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22-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein 22..401
/note= "Mature OCIF-C238"
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"Signal peptide"
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W09626217-A1.
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Synthetic.
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DNA encoding osteoclastogenesis inhibitory factor protein - useful DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 80: Page 126-128; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CEBst in which Gln 371 is substituted by sequence represents OCIF-CEBst in which Gln 371 is substituted by the changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCIF of the invention has a can molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                23-APR-1997 (first entry)
Mutated OCIF, OCIF-CBst.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
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F, Mochizuki S,
Ueda M, Yano K,
                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                 29-AUG-1996, 200374.
20-FEB-1996, J00374.
21-JUL-1995, JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LT GOLO M, Higashio K, Kobayashi F, Nakagawa N, Shima N, Tsuda E, Ue
                    AA.
T 9
R99948 standard; Protein; 393
                                                                                                                                                                         /note= "Signal peptide"
Protein 22.393
/note= "Mature OCIF-CBst"
MISC_difference 392
/label= Gln371Leu
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nes 371; Conservative
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N-PSDB; T33178.
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2; Indels 0; Gaps

Length 401;

Score 2833; DB 20; Pred. No. 1.50e-272; 0; Mismatches

ch 99.0%; l Similarity 99.5%; 378; Conservative

Query Match Best Local Similarity

Matches

22

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/label= sig_peptide
WO9628546-A1.
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N-PSDB; T35475.
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Claim 44; Page 105-107; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCRI in which amino acids 2-42 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 bunder reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg. C, and is lost after 10 mins at 70 deg. G oCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                              61 | YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
                                                                                                                               202 ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrqhssqeqtfqllklwkhqn 261
                                                                                                                                                                                                                                                                                                262 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkvgaediektikackp 321
                                                                                                                                                                                                                                                                                                                                                 241 KDQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutated OCIF, OCIF-DCRI.
Oste¢clastogenesis inhibitory factor; OCIF; heparin; bone resorption;
82|ycspvckelgyvkgecnrthnrvceckegryleiefclkhrscppgfgvvgagtperntv 141
                                                                                                   142 ckrcpdgffsnetsskapcrkhtncsvfgllltgkgnathdnicsgnsestgkcgidvtl 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 88.7%; Score 2539; DB 20; Length 360; Best Local Similarity 98.3%; Pred. No. 1.89e-242; Matches 341; Conservative 1; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-11996;
20-Fgb-1996; J00374.
20-Fgb-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOto M, Higashio K, Kobayashi F, Mochizuki S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c|difference 22.23
te= "Position of deletion, delta 2-42"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "signal peptide"
Protein 22.360
/note= "Mature OCIF-DCR1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goto | M. Higashio K.
Nakagawa N. Shima N.
WPI; |96-402320/40.
N-PSDB; T33166.
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23-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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94 IEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLT 153
                                                                                                                                                        134 qkgnathdnicsgnsestgkcgidvtlceeaffrfavptkftpnwlsvlvdnlpgtkvna 193
                                                                                                                                                                                                                                                                                                         194 esverikrqhssqeqtfqllklwkhqnkdqdivkkiiqdidlcensvqrhighanltfeq 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 lrslmeslpgkkvgaediektikackpsdqilkllslwrikngdddtlkqlmhalkhskt 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 iefclkhrscppgfgvvgagtperntvckrcpdgffsnetsskapcrkhtncsvfglllt 133
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Claim 14; Fig 1; 59pp; Eaglish.

The receptor binds to TNF, and in particular, TNF-beta.

The receptor may be used for screening for antagonists and agonists of the receptor may be used for screening for antagonists and agonists of the receptor and for ligands for the receptor. Such agonists may be used to inhibit the growth of tumours, to stimulate cellular differentiation, to mediate the immune response and anti-viral response, to regulate growth and provide resistance to certain infections. The antagonists may be used therapeutically, to treat autoimmune diseases, inflammation, septic shock, to inhibit graft-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tumour necrosis factor receptor.
Tumour necrosis facor; INF; receptor; INF-beta; ligand; tumour;
differentiation; immune response; autoimmune disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                     214 ESVERIKROHSSQEQTFQLLKLWKHQNKDQDIVKKIIQDIDLCENSVQRHIGHANLTFEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 yhfpktvtgslkktirflhsftmyklygklflemigngvgsvkiscl 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 YHFPKIVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 88.7%; Score 2537; DB 20;
Best Local Similarity 100.0%; Pred. No. 3.03e-242;
Matches 337; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             versus-host reactions, and to prevent apoptosis. Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                septic shock; graft-versus-host; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 11
R99357 standard; Protein; 390 AA.
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15-WAR-1995; U03216.
1E-MAR-1995; WO-U03216.
29-WAR-1995; WO-U03287.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Greene JM;
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ON encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 65; page 119-121; 183pp; Japanese.
Claim 65; page 119-121; 183pp; Japanese.
Claim 65; page 119-121; 183pp; Japanese.
This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CC in which amino acids 331-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 ycspyckelgyvkgecnrthnrvceckegryleiefclkhrscppgfgyvgagtperntv 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                   181 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKROHSSQEQTFQLLKLWKHON 240
                                                                                         202 ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrqhssgegtfgllklwkhgn 261
                                                                      262 kdgdivkkiigdidleensvqrhighanltfeqlrslmeslpgkkvgaediektikackp 321
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Pred. No. 1.63e-236;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morinaga T
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOCO M, Higashio K, Robayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
                                                                                                                                                  322 sdqilkllslwrikngdqdtlkglmhalkhsktyhfp 358
                                                                                                                                                                        301 SDQILKLLSLWRIKNGDQDTLKGLMHALKHSKTYHFP 337
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                              T 12
R99943 standard; Protein; 351 AA.
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                                                                                                                                                                                                                                                                                                 23-APR-1997 (first entry) Mutated OCIF, OCIF-CC.
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Signal peptide"
Protein 22..351
/note= "Mature OCIF-CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-1996.
20-FEB-1996; J00374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96-402320/40.
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                                                                                                                                                                                                                                                                                                                                                           osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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Matches
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to the control of the control, esp. treatment of osteoporosis claim 83; Page 128-129; 183pp; Japanese.

Claim 83; Page 128-129; 183pp; Japanese.

This sequence represents a mutated version of the full length response to the control of the invention. This sequence represents octr-csph in which amino acids 298-380 of the mature sequence represents Octr-csph in which amino acids 298-380 of the mature coult protein are replaced by Ser-Leu-Asp. These changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCTF of the invention has a molecular weight by SDS-PAGE of 60 kD more reducting conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg.C, and is lost resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 ycspyckelgyykgecnrthnrvceckegryleiefclkhrscppgfgyvgagtperntv 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 ckrcpdgffsnetsskapcrkhtncsvfgllltqkgnathdnicsgnsestqkcgidvtl 201
                                                                                                                                                                                23-APR-1997 (first entry)
Musted OCIF, OCIF-CSph.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
osteopocosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 etfppkylhydeetshqllcdkcppgtylkghctakwktvcapcpdhyytdswhtsdecl 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 0; Gaps
262 kdgdivkkiigdidloensvgrhighanltfeqlrslmeslpgkkvgaediektikackp 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding osteoclastogenesis inhibitory factor protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morinaga T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 78.0%; Score 2231; DB 20; Local Similarity 100.0%; Pred. No. 5.85e-211; hes 297; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
                                                                                        322 sdqilkllslwrikngdqdtlkglmhalkh 351
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                         T 13
R99949 standard; Protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                          22..321
"Mature OCIF-CSph"
                                                                                                                                                                                                                                                                                                                      "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-1996.
20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 96-402320/40.
N-PSDB; T33179.
                                                                                                                                                                                                                                                                                                                                                                          WO9626217-A1.
                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                        301
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RESULT

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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 47: Page 107-109: 1838p; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions.

To deg. Cor 30 mins at 56 deg. C, and is lost after 10 mins at 70 deg. Cor 30 mins at 56 deg. C, and is lost after 10 mins at 90 mins the treatment and prevention of disorders of bone resorption, e.g.
                                              Mutated OCIF, OCIF-DCR2. Octeoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 jeiefclkhrscppgfgvvqagtperntvckrcpdgffsnetsskaporkhtncsvfgll 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt tqkgnathdnicsgnsestqkcgidvtlceeaffrfavptkftpnwlsvlvdnlpgtkv\ 190}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 WAESVERIKRQHSSQEQFFQLLKLWKHQNKDQDIVKKIIQDIDLCENSVQRHIGHANLTF 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 eqlrslmeslpgkkvgaediektikackpsdqilkllslwrikngdqdtlkglmhalkhs 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $ikwttq-etfppkylhyde-etshq-llcdk-cppgtylkqhctakwktvcaeckegry 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAKWKTVCAPCPDHY-YIDSWHISDECLYCSPVCKELOYVKQECNRIHNRVC-ECKEGRY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
                                                                                                                                                                                                                                                                                                                       Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2218; DB 20; Length 359;
Pred. No. 1.25e-209;
5; Mismatches 26; Indels 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 ktyhfpktvtqslkktirflhsftmyklyhklflemigngvqsvkiscl 359
                                                                                                                                                                                                                                                                20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
                                                                                                                                                                                      difference 63..64
= "Position of deletion, delta 43-84"
                                                                                                               Location/Qualifiers
R999$7 standard; Protein; 359 AA.
                             23-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 89.4%;
Matches 312; Conservative
                                                                                                                                                                          "Mature OCIF-DCR2"
                                                                                                                                 . 1..21
"Signal peptide"
                                                                                                                                                                                                                                                      996; J00374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 AA;
                                                                                                                                                                                                                                                                                                                                                               N-PSDB; T33167
                                                                                                                                                                                                                    WO9626217-A1.
                                                                               osteóporosis.
                                                                                                                                                                                                                                      966
                                                                                              Synthetic.
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                                                                                                                                                        Protein
                R99937
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No Fabragian Statement of the protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 50, Page 109-111, 183pp, Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents of OCIF-DCRS in which amino acids 85-122 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto action exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C or 30 mins at 66 deg.C, and is lost after 10 mins at 69 control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                              Mutated OCIF, OCIF-DCR3.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 74.1%; Score 2119; DB 20; Length 360; Best Local Similarity 89.9%; Pred. No. 1.60e-199; Matches 339; Conservative 0; Mismatches 0; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 ycspyckelgyvkgecnrthnrvc--------
                                                                                                                                                                                                                                                                                                                                                      Misc_difference 105.106
/note= "Position of deletion, delta 85-122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-1996.
20-FEB-1996; J00374.
20-FEB-1995; JP-207508.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                       Location/Qualifiers
                               (first entry)
                                                                                                                                                                                                                                                                                              Protein 22.360
/note= "Mature OCIF-DCR3"
                                                                                                                                                                                                                                                                  "Signal peptide"
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                               23-APR-1997
                                                                                                                                                                    Synthetic.
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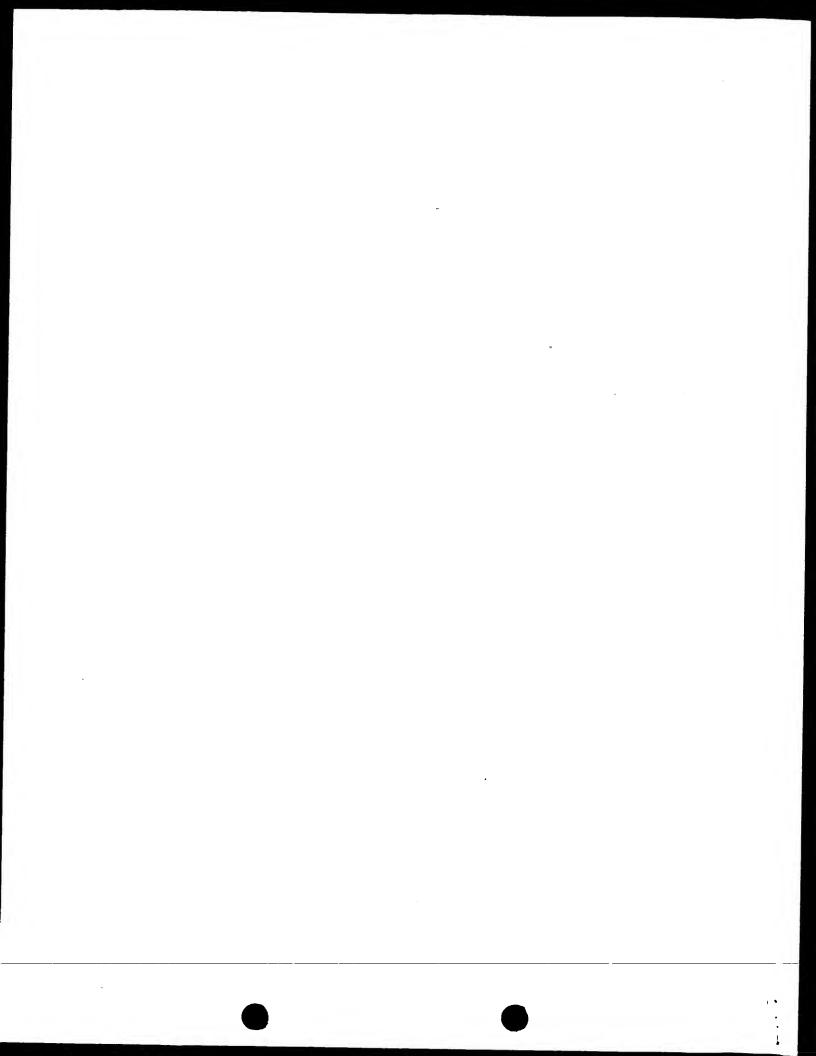
Search completed: Tue Dec 2 14:51:45 1997

qq

R99938 standard; Protein; 360 AA.

RESULT

Job time : 91 secs.



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:48:32 1997; MasPar time 13.77 Seconds 797.024 Million cell updates/sec Run on:

plar output not generated.

>US-08-915-004-4 (1-380) from USO8915004.pep 2861 I ETFPPKYLHYDEETSHQLLC......QKLFLEMIGNQVQSVKISCL 380 litle:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

91006 seqs, 28888923 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:annl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev pir51 Database:

Mean 46.240; Variance 103.115; scale 0.448 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

22 159 5.6 256 14 B32393 T-cell antigen 4-1BB 23 154 5.4 324 14 JC2395 Fes antigen - rat 24 14 5.0 271 14 S12783 OX40 antigen precurs 26 141 4.9 255 13 JT0752 Pmphocyte activation 27 140 4.9 355 13 JT0752 Pmphocyte activation 29 134 4.7 250 2 A49653 Fox antigen precurs 30 134 4.7 315 13 A3142 A50 EDFO antigen precurs 31 124 4.7 315 13 A4065 A50 EDFO antigen precurs 31 124 4.3 103 8 J01791 A558 protein - vacing 4.3 103 8 A42523 Pmphocyte activation 5 105 3.7 28 11 B34576 Pmphocyte activating 36 105 3.7 28 11 B34576 Pmphocyte activating 36 105 3.7 28 11 B34576 Pmphocyte activating 36 105 3.7 31 31 35133 Pmphocyte activating 36 105 3.7 31 31 3513 A84036 A50 EDFO ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATTIVATION ATT	4.60e-08 3.33e-07 3.01e-06 5.61e-06 1.44e-05 1.25e-04 1.25e-04 1.25e-04 1.25e-04 1.25e-04 1.25e-04 1.25e-04 1.35e-03 3.31e-03 3.31e-03 1.31e-01 1.31e-01 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.9
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# ALIGNMENTS

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Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells.
                                                                                                                                                                                        ##cross-references GB:M35857
***Cross-references GB:M35857
**CE A23666
                                 #authors Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6151-6155
Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.
#cross-references Mulb:90349572
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Gene (1994) 150:381-386
Cloning, sequencing and partial functional characterization
of the 5' region of the human p75 tumor necrosis factor
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#product tumor necrosis factor receptor type 2 #status
experimental #label MaT/
#domain NGF receptor repeat homology #label NG1/
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#journal J. Biol. Chem. (1990) 265:1531-1536

Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.
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#binding_site carbohydrate (Asn) (covalent) #status
predicted #molecular-weight 48291 #checksum 5724
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                                                                                                                                                                                                                                                                                                                                                                                                                    ##status preliminary
##molecule_type protein
##residues 23-40;65-69;136-141;300-306 ##label LOE
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sequence extracted from NCBI backbone
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##residues 27-31 ##label ENG
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#map_position 1p36.2-1p36.2
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63; Conservative
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148554 #type fragment
gene muxine tumour necrosis factor receptor 2 protein - mouse
(fragment)
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#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
#fitle Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.
#cross-references MUID:91187885
#accession B38634
45 yydqta-qmccskcspgqhakvfctktsdtvcdscedstytqlwnwypeclscgsrcssd 103
                                                                                                                                                        104 qvetqactreqnrictcrpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckp 163
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Best Local Similarity 41.5%; Pred. No. 3.33e-43;
Matches 66; Conservative 21; Mismatches 61; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #formal_name Mus musculus #common_name house mouse
02-unl-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
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                                      Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A. Mamm. Genome (1994) 5:726-727
Allelic variation of the type 2 tumor necrosis factor
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##molecule_type mRNA
##molecule_type mRNA
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##residues 1-474 ##label LEW
##cross-references GB:M60469
                                                                                                                                                                                                                                              164 capgtfsnttsstdicrphgicnv 187
                                                                                                                                                                                                                                                                                                        124 CPDGFFSNETSSKAPCRKHTNCSV 147
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Characterization of the promoter region of the murine p75-TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #product tumor necrosis factor receptor type 2 #status
                      #authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
#journal Mol. Cell. Biol. (1991) 11:3020-3026
#title Molecular cloning and expression of the type 1 and type 2
murine receptors for tumor necrosis factor.
#drocss.references MuID:91246168
#accession A40254
                                                                                                                                                                                                                                                                                            Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky,
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B-cell activation protein CD40 precursor - human
B-cell surface antigen Bp50
#formal_name Homo sapiens #common_name man
03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in
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#domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG4\
#length 474 #molecular-weight 50319 #checksum 7767
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##residues 1-277 ##label STA
                                                                                                                                                                                                                   1-474 ##label GOO
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##cross-references EMBL:X87128
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NCE A60771
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NCE S54816
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Best Local Similarity 41.5%;
Matches 66; Conservative
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E.A.; Howard, M.; Cockayne, D.A.
J. Immunol. (1992) 149:3921-3926
Genomic structure and chromosomal mapping of the murine CD40
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#map_position 20q12-20q13.2
KEYWORDS B-cell; glycoprotein; phosphoprotein; transmembrane protein
Biochemical characteristics and partial amino acid sequence
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#product B-cell activation protein CD40 #status
experimental #label MAT\
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                         of the receptor-like human B cell and carcinoma antigen {\tt CDw40}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 tsetdtictceegwhctseacescvlhrscspgfgvkqiatgvsdticepcpvgffsnvs 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 NRTHNRVCECKEGRY-L-EI-EFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNET 133
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                                                                                                                                                                                                                                                                                                                                                                                                                            #domain extracellular #status predicted #label EXT\
#domain transmembrane #status predicted #label TMM\
#domain intracellular #status predicted #label CYT\
#binding_site carbohydrate (Asn) (covalent) #status predicted
#length 277 #molecular-weight 30619 #checksum 6261
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B cell-associated surface molecule CD40 - mouse
#formal_name Mus musculus #common_name house mouse
18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
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##experimental_source Burkitt lymphoma cell line Raji
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##residues 1-289 ##label GRI
##cross-references NCBIP:120357
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#accession A46515
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                                                                                                                                                                                                                                                   Torres, R.M.; Clark, E.A. J. Immunol. (1992) 148:620-626 Differential increase of an alternatively polyadenylated mRNA species of mutine CD40 upon B lymphocyte activation.
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77 | NRTHNRVCECKEGRY-L--EIEFCLKHRSCPPGFGVVOAGTPERNTVCKRCPDGFFSNET 133
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#domain NGF receptor repeat homology #label NG3\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
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#journal Virology (1991) 184:370-382
#title Myxoma virus expresses a secreted protein with homology the tumor necrosis factor receptor gene family that contributes to viral virulence.
#cross_references MUID:91335768
                                                                                                                                                Gaps
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T2 protein - myxoma virus (strain Lausanne)
#formal_name myxoma virus
31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                #length 326 #molecular-weight 35208 #checksum 9255
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10.3%; Score 294; DB 14; Length 305;
Best Local Similarity 38.8%; Pred. No. 3.73e-29;
Matches 59; Conservative 20; Mismatches 65; Indels
                               slfekcypwtscedknlevlqkgtsqtnvicg 187
                                                               134 | SSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 165
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                                                                                                                                    #type complete
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##rosidues 1-326 ##label UPT
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CLASSIFICATION #superfamily muvor
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##residues 1-309
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Tumoriganic poxyiruses: genomic organization and DNA sequence of the telomeric region of the Shope fibroma virus genome.
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#title Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid.
#accession 154182
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                                                                                                                                                                                                                                                       30 HNRVCECKEGRY--LE-IEFC-L-KHRS-CPPGFGVVQAGTPERNTVCKRCPDGFFSNET 133
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#formal_name Homo sapiens #common_name man
24 May-1996 #sequence_revision 24 May-1996 #text_change
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B43692 #type complete
12 protein - rabbit fibroma virus
#formal_name rabbit fibroma virus, Shope fibroma virus
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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#domain NGF receptor repeat homology #label NG3
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     Length 326;
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                                                        25; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.41e-23;
31; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 SSKAPCRKHINCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
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Virology (1987) 160:20-30
  Score 269; DB 2;
Pred. No. 4.86e-25;
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1larity 30.5%;
Conservative
Query Match 9.4%;
Best Local Similarity 33.8%;
Matches 47; Conservative
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Matches 51; Conser
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PEBS Lett. (1993) 319:80-83
Genes of variola and vaccinia viruses necessary to overcome
the host protective mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 epghriccsrcppgtyvsakcsrirdtvcatcaensynehwnylticqlcrpcdpv-mgl 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 HQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQE 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 7; Gaps
                                                                                                                 Gaps
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30-Sep-1993 #seguence_revision 30-Sep-1993 #text_change
                                                                                                              Indels 11;
                                ##cross-references GB:L04270; NID:9339761; CDS_PID:9339762 X #length 435 #molecular-weight 46709 #checksum
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                                                                                 Length 435;
                                                                                                                                                                                                                                                                               170 ckaghfqntsspsarcqphtrcenqglveaapgtaqsdttc 210
                                                                                                                                                                                                                                                                                                Score 260; DB 13; L
Pred. No. 1.41e-23;
23; Mismatches 75;
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Pred. No. 8.98e-19;
19; Mismatches 58;
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G4R protein - variola virus
B28R protein (COP)
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Y #length 138 #checksum 6036
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##molecule_type mRNA
##residues 1-435 ##label RES
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Best Local Similarity 35.4%;
Matches 46; Conservative
                                                                                 Query Match 9.1%;
Best Local Similarity 32.3%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           22-Nov-1993
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D36858
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Nucleotides sequence analysis of the region of variola virus
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gene name TNFR-2
#length 454 #molecular-weight 50030 #checksum 4267
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#title Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.
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#formal_name Mus musculus #common_name house mouse
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
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                              ##experimental_source strain India-1967, ssp. major, isolate Ind3
NCE
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#domain NGF receptor repeat homology #label NG3
#length 349 #molecular-weight 38189 #checksum 2016
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##cross.references EMBL:X67117
##experimental_source strain India-1967, isolate Ind3
FECATION #superfamily NGF receptor repeat homology
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Pred. No. 8.98e-19;
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##cross-references GB:X69198
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Best Local Similarity 35.48;
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##residues 1-4
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#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.

#cross-references MUID:91187885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
#journal Bur. J. Immunol. (1991) 21:1649-1656
#title Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.
#cross-references MUID:91285014
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Nucleotide sequence of the TNF type I receptor from a mouse
endothelioma cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
#journal Mol-Cell. Biol. (1991) 11:3020-3026
#title Molecular cloning and expression of the type 1 and type 2
murine receptors for tumor necrosis factor.
#cross-references MUID:91246168
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Immunogenetics (1991) 34:338-340
Molecular cloning and expression of the mouse Inf receptor
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##cresidues 1-454 ##label RES
##cressreferences GB:L26349; NID:9430732; CDS_PID:9430733
This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
FICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
                                                                                                                                                                                          tumor necrosis factor receptor type 1 precursor - mouse tumor necrosis factor receptor, 55K #formal-name Mus musculus #common_name house mouse 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Oct-1996
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                                               123 RCPDGFFSNETSSKA-P-CRKHINC 145
                  168 -chagfflresecvpcshckkneec 191
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##residues 1-454 ##label LEW
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##residues 1-454 ##label ROT
##cross-references EMBL:X57796
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tumor necrosis factor receptor type 1 precursor - rat
tumor necrosis factor binding protein 1 (TNF blocking factor)
#formal_name Rattus norvegicus #common_name Norway rat
30-Jun-1992 #sequence_revision 07-oct-1994 #text_change
05-Apr-1995
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#product tumor necrosis factor receptor type 1 #status
predicted #label MAT\
#domain extracellular #status predicted #label EXT\
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#product tumor necrosis factor receptor type 1 #status
predicted #label MAIY
#domain extracellular #status predicted #label EXT\
#product tumor necrosis factor binding protein #status
predicted #label TBP\
#domain NGF receptor repeat homology #label NG1\
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duplication; glycoprotein; receptor; transmembrane protein
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N #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology duplication; glycoprotein; receptor; transmembrane protein
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#title Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 ywhsknnsicctkchkgtylvsdcpspgrdtvcrecekgtftasgnylrgclscktcrke 108
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#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG3\
#domain transmembrane #status predicted #label NG4\
#domain intracellular #status predicted #label NF1\
#length 454 #molecular-weight 50129 #checksum 4839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 YDEETSHOLLCDKCPPGTYLKOHCTAK-WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.33e-17;
21; Mismatches 65; Indels 11; Gaps
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##residues 1-461 ##label HIM
##cross-references GB:M63122
VI This protein is one of two known receptors for both TNF-alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 454;
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Best Local Similarity 33.1%;
Matches 48; Conservative
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235-461
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236-454
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127-167
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168-204
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84-126
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sidues 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416
##label HEU

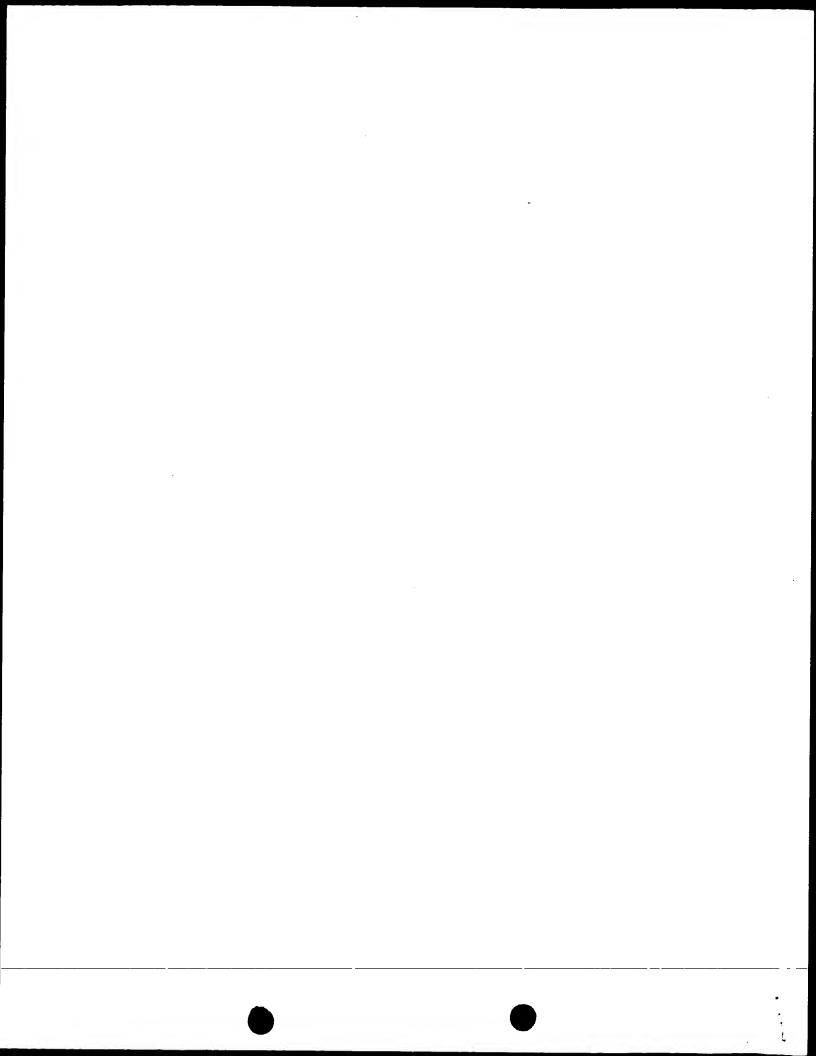
This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells, and on a variety of nonneuronal derivatives of the neural crest.

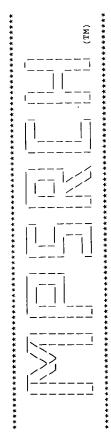
The cysteine rich region of the extracellular domain may form part or all of the NGF-binding site.

This protein is thought to form a high-affinity receptor when it associates with the 140K frk proto-oncogene, which contains an intracellular tyrosine kinase domain.

TION #superfamily nerve growth factor receptor; NGF receptor
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#product nerve growth factor receptor #status predicted
#label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M. Dev. Biol. (1990) 137:287-304
Structure and developmental expression of the chicken NGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reichardt, L.F.
#journal Neuron (1989) 2:1123-1134
#title Structure and developmental expression of the nerve growth factor receptor in the chicken central nervous system.
#cross-references MUID:90166579
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#region cysteine-rich\
#domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG3\
#comain NGF receptor repeat homology #label NG4\
#region scrinc/threonine-rich\
#comain transmembrane #status predicted #label MEN\
#domain intracellular #status predicted #label INT\
#binding_site carbohydrate (Asn) (covalent) #status
                                                     Gaps 10;
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                                                                                                                                                                                                                                                  49 yahpknnsicctkchkgtylvsdcpspggetvcevcdkgtftasgnhvrgclscktcrke 108
                                                                                                                                                                                                             109 mfqveispckadmdtvcgckknqfqrylsethfqcvdcspcfng-tvtipckekqntvcn 167
                                                                                                                                                           10 YDEETSHQLLCDKCPPGTYLKQHCTAK-WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JN0006 #type complete
nerve growth factor receptor, low affinity - chicken
NGF receptor
#formal_name Gallus gallus #common_name chicken
05-Apr.1990 #sequence_revision 07-Jun-1990 #text_change
JN0006; A60504
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Score 220; DB 2; Length 461;
Pred. No. 3.34e-17;
22; Mismatches 63; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
##residues 1-416 ##label LAR
#experimental source embryonic chick brain
ENCE A60504
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                                                                                                                                                                                                                                                                                                                            168 -chagfflsgnectpcshckkngec 191
Query Match 7.7%;
Best Local Similarity 33.8%;
Matches 49; Conservative
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240-261
262-416
52
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21-182
24-57
59-100
101-139
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                                                                                                                                               20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHY-YTDSWHTSDECLYCSPVCKELQYVKQECNR 78
                                                                                 Gaps
predicted #molecular-weight 44654 #checksum 3542
                                              Length 416;
                                              Score 215, DB 6, Length 416 Pred. No. 2.01e-16; 27; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                      Search completed: Tue Dec 2 14:49:58 1997 Job time: 86 secs.
                                                                                                                                                                                                                                                    154 dpclpcticeenevmvke-ctatsdaec 180
                                                                                                                                                                                                                                                                                      137 APCRKHINCSVFGLLLIQKGNATHDNIC 164
                                              Query Match
Best Local Similarity 30.4%;
Matches 45; Conservative
                 SUMMARY
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Dec 2 14:47:03 1997; MasPar time 9.74 Seconds 827.678 Million cell updates/sec Run on:

ular output not generated.

Title:

>US-08-915-004-4 (1-380) from US08915004.pep 2861 I ETFPPKYLHYDEETSHQLLC......QKLFLEMIGNQVQSVKISCL 380 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 48.034; Variance 81.732; scale 0.588 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ					
Result No.	Score	Query	Length	DB	ΩI	Description	Pred. No.
	405	14.2	461	. 6	TNR2 HUMAN	TUMOR NECROSIS FACTOR	6.30e-63
10	375	100	474	σ.	TNR2 MOUSE	TUMOR NECROSIS FACTOR	3.56e-56
1 (*	303	10.6	277	~	CD40_HUMAN	CD40L RECEPTOR PRECUR	2.64e-40
4	294	10.3	289	7	CD40 MOUSE	CD40L RECEPTOR PRECUR	2.31e-38
ינר	269	4.6	326	10	VT2 MYXVL	TUMOR NECROSIS FACTOR	5.03e-33
· w	265	6.9	415	σ	TNRC_MOUSE	LYMPHOTOXIN-BETA RECE	3.52e-32
7	260	9.1	325	10	VT2_SFVKA	TUMOR NECROSIS FACTOR	3.98e-31
. α	260	9.1	435	σ	TNRC HUMAN	LYMPHOTOXIN-BETA RECE	3.98e-31
σ		0	349	10	VC22 VARV	PROTEIN C22/B28 HOMOL	6.59e-25
, 0		7.7	454	5	TNR1 MOUSE	TUMOR NECROSIS FACTOR	4.45e-23
1.	220	7.7	461	σ	TNR1_RAT	TUMOR NECROSIS FACTOR	7.09e-23
12		7.5	416	9	NGFR CHICK	LOW-AFFINITY NERVE GR	7.20e-22
	213	7.4	427	φ	NGFR HUMAN	LOW-AFFINITY NERVE GR	1.81e-21
14	207	7.2	425	φ	NGFR RAT	LOW-AFFINITY NERVE GR	2.85e-20
. 1.	188	9.9	323	•	FASA_BOVIN	FASL RECEPTOR PRECURS	1.51e-16
9	186		461		TNR1_PIG	TUMOR NECROSIS FACTOR	3.67e-16
17	178		595	7	CD30_HUMAN	CD30L RECEPTOR PRECUR	1.24e-14
1.0			455		TNR1_HUMAN	TUMOR NECROSIS FACTOR	1.67e-13
0	-	10	256	Н	41BB MOUSE	4-1BB LIGAND RECEPTOR	4.22e-11
100	٠,-		260	7	CD27 HUMAN	CD27L RECEPTOR PRECUR	4.22e-11
2.5	146		271	7	OX40 RAT	OX40L RECEPTOR PRECUR	8.91e-09
22	144	5.0	272	7	OX40 MOUSE	OX40L RECEPTOR PRECUR	2.00e-08

9.85e-08 3.22e-08 3.22e-08 1.04e-06 1.04e-06 1.04e-05 4.67e-03 1.24e-03 1.24e-03 1.49e-01 1.49e-01 1.49e-01 1.49e-01 1.33e-01 3.30e-01 3.33e-01 7.33e-01	
4-18B LIGAND RECEPTOR OXAOL RECEPTOR PRECURE FASL RECEPTOR PRECURS PROTEIN A53.  PROTEIN A53.  PROTEIN A53.  HYPOTHETICAL 41.6 KD CAMP-REGUIAED D2 PROTEIN A53.  HYPOTHETICAL 41.6 KD CAMP-REGUIAED D2 PROVON WILLEBRAND FACTOR ILAMININ ALPHA-1 CHAIN GLUCOSAMINE-FRUCTOSE HYPOTHETICAL 128.8 KD DESMOPLAKIN I AND II PROTHETICAL 128.8 KD DESMOPLAKIN I AND II PROCHAME SYNTHETASE CHROMOSOME ASSEMBLY PROMOSOME ASSEMBLY PROCHAM HEAVY CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN	MICSIN BEAVI CRAIN C BASEMENT MEMBRANE-SPE DYNEIN HEAVY CHAIN, C
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2555 2777 2277 2277 2277 2281 3081 3081 31122 4310 4310 4411 1120 1120 1120 1120 1120 1120 11	194 / 3707 4092
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# ALIGNMENTS

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SAPIENS (HUMAN)
                            EUTHERIA; RODENTIA.
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474 AA;
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SEQUENCE
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           yydqta-qmccskcspgqhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcssd 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 QYVKQECNRTHNRVCECKEGRY--LEI-EFC-L-KH-RSCPRGFGVVQAGTPERNTVCKR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 6.30e-63;
26; Mismatches 59; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR RECEPTOR 2. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWR2_MOUSE STANDARD; PRT; 474 AA.

125119; 1192 (REL. 22, CREATED)
01-MAY_1992 (REL. 22, LAST SEQUENCE UPDATE)
01-MAY_1996 (REL. 34, LAST SEQUENCE UPDATE)
10-CGT_1996 (REL. 34, LAST ANNOTATION UPDATE)
10-MON NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 405; DB 9; Length 461;
                                                                                                                                                                                                                                                      PROSIȚE; PS00652; TNFR_NGFR.
RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capgtfsnttsstdicrphqicnvvai---p-gnasrdavctsts 204
                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R -> P (IN REF. 3).

R -> M (IN REF. 1).

A -> T (IN REF. 3).

OF5DOC44 CRC32;
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TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
J. BĻOL. CHEM. 267:21172-21178(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.2%;
                                                                                                  M32315; G189186; -. M35857; G339752; -. M55994; G339758; -.
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Conservative
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196
363
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143
161
179
171
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67
75
                                                                                                                                                A35356; A35356.
A36007; A36007.
A36475.
B3610; B35010;
A23666; A23666.
P19438; ITNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
196
363
461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les | 69; Conserv
                                                                                                                                                                                                                        HSSP; P19438
MIM; 191191;
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TRANSMEM
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CONFLICT
SEQUENCE
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REPEAT
REPEAT
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EMBL;
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                                                                                                                                                  PIR;
PIR;
PIR;
PIR;
PIR;
                                                                                                                                    EMBL;
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CD40_HUMAN STANDARD; PRT; 277 AA.

CD40_HUMAN
1925942 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-UUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (CDM40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 gmccakcppggyvkhfcnktsdtvcadceasmytgvwngfrtclscssscttdgveirac 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 tkggnrvcaceagrycalkthsgscrgcmrlskcgpgfgvassrapngnvlckacapgtf 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 375; DB 9; Length 474;
Pred. No. 3.56e-56;
21; Mismatches 61; Indels 11; Gaps
                                                                                                                                                                                         MEDLINE; 91246168.

MEDLINE; 91246168.

GOODNIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
COPELAND N.G., JENKINS N.A., SMITH C.A.;
MOL. CELL. BIOL. 11:3020-3026(1991).
-!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
-!- SUBCELDULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR RECEPTOR 2.
                                                         SEQUENCE FROM N.A.
MEDLINE; 91187885.
LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.
WONG G.H., CHEN E.Y., GOEDDEL D.V.,
PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P19438; ITNR.
PROSITE; PS00652; INFR_NGFR.
RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DC32B2B6 CRC32;
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TNFR-CYS 1.
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TNFR-CYS 3.
TNFR-CYS 4.
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163
181
181
69
195
PC
195
PC
195
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Local Similarity 41.5%;
les 66; Conservative
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EMBL; M59378; G202095; -.
PIR; B38634; B38634.
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DOMAIN
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DOMAIN
REPEAT
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01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (EP50) (CDW40).
                                                                                                                                                                                                                                                                                                                                                                        96 tsetdtictceegwhctseacescvlhrscspgfgykqiatgysdticepcpygffsnvs 155 ::| | | | | | | | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                    38 cslcqpgqklvsdctefteteclpcgesefldtwnrethchqhkycdpn-lglr-vqqkg 95
                                                                                                                                                                                                                                                                                                                                               20 CDKCPPGTYLKQHCTAKWKIVCAPCPDHYYTDSWHTSDEC-L--YCSPVCKELQYVKQEC 76
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                          -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
BELL: X60592; G29851; -.
PIR: S04460; S04460.
MIM; 109535; -.
                                                                                                                                                                                                                                                                                                                  ώ
ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                   PROSITE; PS00652; INFR_NGFR.
RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
                          SEQUENCE FROM N.A.
MEDLINE; 89356608.
MEDLINE; 89356608.
SAPAMNINOVIC I., CLARK E.A., SEED B.;
EMBO J. 8:1403-1410(1989).
-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEĞUENCE FROM N.A.
STARAN-BALBAC; TISSUB-LIVER;
MEDLINE: 9309458
GRIMALDI J.C., TORRES R., KOZAK C.A., CHANG R., CLARK E.A.,
                                                                                                                                                                                                                                                                                            Score 303; DB 2; Length 277; Pred. No. 2.64e-40;
                                                                                                                                                                                                                                                                                                                21; Mismatches 67; Indels
                                                                                                                                                                CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C;
TORRES R.M.;
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                          3B284411 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 AA
                                                                                                                                                                                                       4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                156 safekchpwtscetkdlvvqqagtnktdvvcg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                   134 SSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 165
                                                                                                                                                                                                                         TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
POTENTIAL.
                                                                                                                                                                                                                  TNFR-CYS 1
                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE, 92105763.
TORRES R.M., CLARK E.A.;
J. IMMUNOL. 148:620-626(1992).
                                                                                                                                                                                                                                                                          30619 MW;
                                                                                                                                                                                                                                                                                             10.6%;
36.8%;
                                                                                                                                                                                                                                                                                                                 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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153
180
277 AA;
          EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD40_MOUSE
P27512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS
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TRANSMEM
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                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                        SIGNAL
                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                 Matches
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L UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;

RL VIROLOGY 184:370-382(1991).

CC -I FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO CC REACL CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.

CC -I SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. DR RMBL; M92181; G332310; -.

DR PRBL; A40566; GQVZML.

DR HSSP: P19438; ITRR.

NR PROSITE; PSOURE.

NR PROSITE; PSOURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 taesdtvctckegghctskdceacaghtpcipgfgvmematettdtvchpcpvgffsngs 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 cdlcqpgsrltshctalektqchpcdsgefsaqwnreirchqhrhcepn-qglr-vkkeg 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKELQYVKQEC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Gaps
MYXOMA VIRUS (STRAIN LAUSANNE).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                         PROSITE; PS00652; TNFR_NGFR.
RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR'(PROTEIN T2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 294; DB 2; Length 289,
Pred. No. 2.31e-38;
20; Mismatches 65; Indels
                                                                                                                                                                                                                                                         CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                       COUNTY OF THE CYS.

4 X THER-CYS.
THER-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                D8D70A2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 X TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 slfekcypwtscedknlevlqkgtsqtnvicg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFR-CYS 2.
INFR-CYS 3.
TNFR-CYS 4.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSO0652; INFR_NGFR.
GLYCOPROTEIN; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN T2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  32111 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match
Local Similarity 38.8%;
nes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16
326
186
                                                                                                                                                                       PIR; A46476; A46476.
HSSP; P19438; 1TNR.
PROSITE; PS00652; TNI
                                                                                                                                                                                                                                                         LT 5
VT2_MYXVL
P29825;
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9

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VT2_SFVKA
P25943;
          DISULFID
                           DISULFID
                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                             CARBOHYD
                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                              Matches
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    FT FT FT FT SO STA
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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL: L38423; G600223; -.
EMBL; U30798; G1061327; -.
                                                                                                                                                     100 rdrvcdcsagnycllkgqegcricapktkcpagygvs-ghtrtgdvlctkcprytysdav 158
                                                                                                                                                              20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYIDSWHTSDECLYCSPVCKELQYVKQECNRT 79
                                                                                                                      40 ctscppgsyasrlcgpgsdtvcspcknetftastnhapacvscrgrctghlsesgscdkt 99
                                                                                                      9; Gaps
                                                                                                                                                                                                                                                                                                                                           STRAİN=CVB; TISSUE-LUNG;
FORCE W.R., WILLIAMS-ABBOTI L., BROWNING J., HESSION C., TIZARD R.,
                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKRAYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; RODENTIA.
                                                                                    Length 326;
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE: 96163885.
NAKAMURA T., TASHIRO K., NAZAREA M., NAKANO T., SASAYAMA S. HONJÓ T., GENOMICS 30:312-319(1995).
                                                                                            Pred. No. 5.03e-33;
25; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
LYMPHOTOXIN-BETA RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X THER-CYS.
THER-CYS 1.
THER-CYS 2.
THER-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U30798; G1061327; -.
RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                    DB 10;
                                                                     2F059A61 CRC32;
                                                                                                                                                                                                                                                       01-0¢T-1996 (REL. 34, CREATED)
01-0¢T-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0¢T-1996 (REL. 34, LAST ANNOTATION UPDATE)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                         415 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
TNFR-CYS 1.
TNFR-CYS 3.
TNFR-CYS 4.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                     Score 269;
                                                                    35208 MW;
                                                                                                                                                                                                       134 SSKAPCRKHTNC-SV-FGL 150
                                                                                                                                                                                      159 sstetctssfnyisvefnl 177
                                                                                    Query Match
Best Local Similarity 33.8%;
Matches 47; Conservative
                                                                                                                                                                                                                                         STANDARD;
  62
1104
1147
1186
1181
205
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
205
238
326 AA;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

\begin{array}{c|c}
\text{LT} & 6 \\
\text{TNRC} & \text{MOUSE} \\
\text{P50284};
\end{array}

                                  CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                    SECUENCE
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DISULFID
                                                           CARBÓHYD
 REPEAT
REPEAT
REPEAT
                         REPEAT
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A MELLINE; 91207415.

A MITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARRAH T., UPTON C.,

A MCFADDEN G., GOODWIN R.G.;

BIOCHEM BIOPHYS. RES. COMMIN. 176:335-342(1991).

- I- FUNCTION: BINDS TO THE-ALPHA AND BETA. PROBABLY PREVENTS THE TO REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL

- RANIVIRAL EFFECTS OF THE CYTOKINE.

- I- SIMILARITY: CONTAINS A LA-NGFK/TNFR-TYPE CYSTEINE-RICH REGION.

BENBL, A33727; E199408; -.

DR REML, A33727; E199408; -.

BIR; B43692; B43692.

RHSSP, P19438; JINR.

PROSITE; PSO0652; TNFR_NGFR.

KW PREEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                     52 epmhdvccsrcppgefvfavcsrsqdtvcktcphnsynehwnhlstcqlcrp-cdivlgf 110
                                                                                                                                                                                                                                                                                                                                                                          111 eevapctsdrkaecrcqpgmscvyldnecvhceeerlvlcqpgteaevtdeimdtdvncv 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 pckpghfqntssprarcqphtrceigglveaapgtsysdticknppepgamlllaills1 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTLCE 182
                                                                                                                                                                                                                                                                                                                                                                                                               72 VK-QECNRTHNRVCECKEGR---YLEIE--FCLKHR-S-CPPGFGV-VQAGTPERNTVCK 122
                                                                                                                                                                                                                                                                                                               13 ETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE-LQY 71
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
LEPORIPOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
                                                                                                                                                                                                Score 265; DB 9; Length 415;
Pred. No. 3.52e-32;
30; Mismatches 92; Indels 11;
                                                                                                                                  POTENTIAL.
3C5DD121 CRC32;
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
PROTEIN T2.
4 X INFR-CYS.
INFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILINE; 87321103.
UPTON C., DELANGE A.M., MCFADDEN G.;
VIROLOGY 160:20-30(1987).
                                                                                                                                                       MW.
                                                                                                                                                                                                   9.38;
                                                                                                                                                                                                                     larity 28.9%;
Conservative
124
132
150
169
187
40
179
44956 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1865
1867
1986
1986
1986
1987
1981
1981
2083
                                                                                                         40
179
415 AA;
                                                                                                                                                                                                                     Local Similarity
nes 54; Conser
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                                                                                                                         100 hdrvcncstgnycllkgqngcricapqtkcpagygvs-ghtragdtlcekcpphtysdsl 158
                                                                              20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRT 79
                                                                 40 caschpgfyåsrlcgpgsntvcspcedgtftastnhapacvscrgpctghlsesqpcdrt 99
                                                                                                                                                                                                                                936941;
01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94225209.

WEDLINE; 94225209.

COOME PL., VAN ARSDALE T.L., WALTER B.N., WARE C.F., HESSION C., EHRUNELS B., BROWNING J.L., DIN W.S., GOODWIN R.G., SMITH C.A.; SCIENCE 264:707-710(1994).
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMUNE DEVELOPMENT.
-- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
--- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; L04270; G339762; -.
                                                                                                                                                                                                                                                                                                                                                                                           BAENS M., CHAFFANET M., CASSIMAN J.J., DEN BERGHE H., MARYNEN P.;
GENOMICS 16:214-218(1993).
                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKRRYOTA: METAZOA; CHORDATA; VERTEBRATA: TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                            .;
œ
                       Length 325;
                                           Indels
                                                                                                                                                                             134 SSKAPCRKHINCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
                                                                                                                                                       sptercgtsfnyisvgfnlypvnetscttt-aghneviktkeftvtl 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYMPHOTOXIN-BETA RECEPTOR EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P19999; ICLG.
PROSITE; PS00652; TNFR_NGFR.
RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                           31; Mismatches 77;
                    9.1%; Score 260; DB 10;
larity 30.5%; Pred. No. 3.98e-31;
Conservative 31; Mismatches 77;
325 AA; 35132 MW; C9D2C87B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PY SIMILARITY.
PY SIMILARITY.
PY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                         435 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNFR-CYS
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2227
2248
435
2111
2111
24
1124
728
80
80
980
1116
1124
1132
1147
1185
                               Best Local Similarity
Matches 51; Conser
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 93252381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 600979; -.
                                                                                                                                                                                                              RESULT 8
THRC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
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DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
 SEQUENCE
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                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: CONTAINS TWO LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
EMBL; X651198; G457087; -.
EMBL; X65119; G516449; -.
PIR: D36558; D5558.
PIR: S35987; S35987.
PIR: S46888; S46888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 cntthnricecspgyycllkgssgckacvsqtkcgigygvs-ghtsvgdvicspcgfgty 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 CNRTHNRYCECKEGRY--LE--IE--FCLKHRSCPPGFGVVQAGTPERNTYCKRCPDGFF 129
                                                                                                                                                                                                                                                                              13 ETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 hnlcclscppgtyasrlcdsktntqctpcgsgtftsrnnhlpaclscngrcnsnqvetrs 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 HQLLCDKCPPGTYLKQHCTAKWKTYCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIOLA VIRUS.
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                       Score 260; DB 9; Length 435;
Pred. No. 3.98e-31;
23; Mismatches 75; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 10; Length 349; 6.59e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 ckaghfqntsspsarcqphtrcenqglveaapgtagsdttc 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 CPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHCHELKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;
FEBS LETT. 319:80-83(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 108 2 X TNFR-CYS.

31 66 TNFR-CYS 1.

67 108 TNFR-CYS 3.

349 AA; 38189 MW; 500B435 CRC32;
   177 177 POTENTIAL.
435 AA; 46709 MW; 203B82DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-INDIA-1967 / ISOLATE IND3;
MEDLINE; 93202281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00652; TNFR_NGFR.
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Local Similarity 35.4%;
                                                                                          / Match 9.1%;
Local Similarity 32.3%;
nes 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN C22/B28 HOMOLOG
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VC22_VARV
P34015;
CARBOHYD
SEQUENCE
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DT 01
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01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (INF-R1) (P55).
TUFRH OR TUFR-1.
                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 91285014.
BARREDT K., FELDMANN M., FOXWELL B.M.J., KISSONERGHIS A.M., GRAF P.W., FELDMANN M., FOXWELL B.M.J.;
EUR. J. IMMUNOL. 21:1649-1656(1991).
                        MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMOR NECROSIS FACTOR RECEPTOR 1. EXTRACELLULAR (POTENTIAL).
                                                                                                          MEDLINE; 91246168.
GOODMIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I., COPELLAND N.G., JENKINS N.A., SMITH C.A.;
MOL. (CELL. BIOL. 11:3020-3026(1991).
                                                     SEQUENCE FROM N.A.
MEDLINE: 91187885.
LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
WONG G.H., CHEN E.Y., GOEDDEL D.V.;
PROC., NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X INFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                        TISSUE-SPLEEN,
MEDLINE; 92039915.
ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
IMMUNGGENETICS 34:338-340(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
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TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 91246168.
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TRANSMEM
DOMAIN
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REPEAT
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MEDLINE, 91090841.

A HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
A HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
A HIMMLER A., OLSON I., HADDMANN R., STRAIOWA C., ADOLF G.R.;
DNA CELL BIOL. 9:705-7151990.

- !- FUNCTION: RECEPTOR FOR TNF-ALPHA.
- !- SUMLCHAIN: COMTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

- RMBL; M63122, G207362.
- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

- PROSITE; P80655; B16555
- RSSP; P19438; 11NR.

- PROSITE; P806652; TURR_NGRAIN: GLYCOPROTEIN; REPEAT; SIGNAL.
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                                                                                                                                                                                                49 yvhsknnsicctkchkgtylvsdcpspgrdtvcrecekgtftasqnylrqclscktcrke 108
                                                                                                                                                                                                                                                              69 LOYVK-QECNRTHNRVCECKEG --- RYL-EIEF-CLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                             10 YDEETSHOLLCDKCPPGTYLKQHCTAK-WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                    Score 221; DB 9; Length 454;
Pred. No. 4.45e-23;
21; Mismatches 65; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                      01-AGG-1991 (REL. 19, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (INF-R1) (P55).
                                                                                                                                                                                                                                                                                                                                                                                                                           RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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4B6EEC09 CRC32;
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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Local Similarity 33.1%;
les 48; Conservative
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454 AA;
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TNR1_RAT
P22934;
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TRANSMEM
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
GALLIFORMES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 mfqveispckadmdtvcgckknqfqrylsethfqcvdcspcfng-tvtipckekqntvcn 167
                                                                                                                                                                                                                                                                                                                                                                                                                             10 YDEETSHQLLCDKCPPGTYLKQHCTAK-WKTYCAPCPDHYYTDSWHISDECLYCSPYCKE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEUER J.G., FATEMIE-NAINIE S., WHEELER E.F., BOTHWELL M.;
DEV. BIOL. 137:287-304(1990).
-!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
NT-3, AND NT-4.
-!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
                                                                                                                                                                                                                                                                                                                                               22; Mismatches 63; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LARGE T.H., WESKAMP G., HELDER J.C., RADEKE M.J., MISKO T.P., SHOOTER E.M., REICHARDI L.F.; NEURON 2:1123-1134(1989).
                                                                                                                                                                                                                                                                                                 Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGF RECEPTOR. EXTRACELLULAR (POTENTIAL).
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4 X THER-CYS
THER-CYS 1.
THER-CYS 2.
                                                                                                                                                                                                                                                                                              Score 220; DB 9;
Pred. No. 7.09e-23;
                                                                                                                                                                                                                        POTENTIAL.
82F68B08 CRC32;
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(REL. 16, LAST SEQI
(REL. 32, LAST ANN
                                                                                                                                                                                                                                                50969 MW;
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Local Similarity 33.8%;
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                       143
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01-NOV-1990
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P18519;
DISULFID
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94 sddavcrcaygyfqdelsgsckecsicevgfglmfpcrdsqdtvceecpegtfsdeanfv 153
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1-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANDATION UPDATE)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-:- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
-:- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
BIR; A25218; GQHUN.
HSSP; P19438; ITNR.
MIM; 162010; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE: 87051725.
JOHNSON D., LANHAN A., BUCK C.R., SEHGAL A., MORGAN C., MERCER E BOTHWELL M., CIRAO M.;
CELL 47:545-554(1986).
-! FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3, AND NT-4.
SUBUNT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                               .
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO0652; INFR_NGFR.
PROSITE; PSS0017; DEATH_DOMAIN.
RECEPTOR. NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; PHOSPHORYLATION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                  Length 416;
                                                                                                                                                                                                                                                                                                                                  Score 215; DB 6; Length 416 Pred. No. 7.20e-22; 27; Mismatches 70; Indels
                                                                                                                                                                                                                                            C -> Y (IN REF. 2).
T -> K (IN REF. 2).
N -> S (IN REF. 2).
K -> R (IN REF. 2).
4D3F086A CRC32;
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                         SER/THR-RICH.
DEATH DOMAIN.
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Y -> K (IN REF.
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Local Similarity 30.4%;
es 45; Conservative
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P08138;
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PHOSPHORYLATION; SIGNAL
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FASA_BOVIN
P51867;
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                                                                                                                                                                                                                                                                          20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHY-YTDSWHISDECLYCSPVCKELQYVKQECNR 78
                                                                                                                                                                                                                                                  5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-LIVER;
MEDLINE: 93077038.
MEDLINE: 93077038.
METSIE M., ITMUGNET., ALLIKMETS R., SAARMA M., PERSSON H.;
GENE 121:247-254(1992).
-i- PÜNCITON: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
NT-3, AND NT-4.
-i- SÜBUNIT: NGF RECEPTOR CAN FORM A HOWODIMER THROUGH DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RADEKD M.J., MISKO T.P., HSU C., HERZENBERG L.A., SHOOTER E.M.;
NATURE 325:593-597(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOND FORMATION.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PIM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATTU'S NORVEGICUS (RAT).
EUKARKOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                               Score 213; DB 6; Length 427;
Pred. No. 1.81e-21;
19; Mismatches 60; Indels
                EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                          4 X INFR-CYS.
                                                                                    DEATH DOMAIN.
          RECEPTOR
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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ilarity 34.9%;
Conservative
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Local Similarity
nes 45; Conserv
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427 AA;
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MEDLINE; 87115859.
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                DOMAIN
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NGFR_RAT
P07174;
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MEDLINE; 96226401.
YOO J., STONE R.T., BEATTIE C.W.;
DNA CELL BIOL. 15:227-234(1996).
-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. MEDIATES
CELL DEATH. FAS-MEDIATED APOPIOSIS MAY HAVE A ROLE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (REL. 34, CREATED)
1-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
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BOS TAURUS (BOVINE).
EUKRRYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACIYLA.
                     EMBL; X05137; G56756; -.
EMBL; X61269; -; NOT_ANNOTATED_CDS.
PIR; A26431; A26431.
HSSP: p19438; 1TNN.
PROSITE; PS00652; TUNR NGFR.
PROSITE; PS50017; DEATH_DOMAIN.
RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLXCOPROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 207; DB 6; Length 425;
Pred. No. 2.85e-20;
21; Mismatches 60; Indels
                                                                                                                                                                                                                                 NGF RECEPTOR. EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 X INFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
SER/THR-RICH.
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Best Local Similarity 33.3%;
Matches 43; Conservative
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US-08-915-004-7.rag

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 3 10:07:14 1997; MasPar time 2.12 Seconds 86.963 Million cell updates/sec

ular output not generated.

Title: >US-08-915-004-7
Description: (1-15) from US08915004.pep
Perfect Score: 113

Sequence: 1 ETFPPKYLHYDEETS 15

Scoring table: PAM 150

Searched: 101610 seqs, 12294212 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq28 |:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 | 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 | 14:part14 15:part15 16:part16 17:part17 18:part18 | 19:part19 20:part20 21:part21

Statistics: Mean 19.020; Variance 64.466; scale 0.295

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Sult No.	Score	Query Match	Length	DB	ΩI	Description	Pred. No
	113	100.0	15	20	R99926	Osteoclastogenesis in	6.54e-05
7	113	100.0	84	20	R99951	Mutated OCIF, OCIF-CP	6.54e-05
m	113	100.0	106	20	R99947	Mutated OCIF, OCIF-CC	6.54e-05
4	113	100.0	143	20	R99946	Mutated OCIF, OCIF-CC	. 54
ഹ	113	100.0	145	20	R99930	Osteoclastogenesis in	6.54e-05
9	113	100.0	154	20	R99929	Osteoclastogenesis in	6.54e-05
7	113	100.0	187	20	R99950	Mutated OCIF, OCIF-CB	6.54e-05
ω	113	100.0	197	20	R99945	Mutated OCIF, OCIF-CD	6.54e - 05
6	113	100.0	272	20	R99944	Mutated OCIF, OCIF-CD	6.54e-05
10	113	100.0	321	20	R99949	Mutated OCIF, OCIF-CS	6.54e-05
11	113	100.0	326	20	R99940	Mutated OCIF, OCIF-DD	6.54e-05
12	113	100.0	327	20	R99941	Mutated OCIF, OCIF-DD	6.54e-05
13	113	100.0		20	R99943	Mutated OCIF, OCIF-CC	6.54e-05
14	113	100.0	m	20	R99937	Mutated OCIF, OCIF-DC	6.54e-05
15	113	100.0	m	20	R99939	Mutated OCIF, OCIF-DC	6.54e-05
16	113	100.0	36	20	R99938	Mutated OCIF, OCIF-DC	6.54e-05
17	113	100.0	380	20	R99924	Mature osteoclastogen	6.54e-05
18	113	100.0	390	20	R99357	Human tumour necrosis	6.54e-05
19	113	100.0	393	20	R99948	Mutated OCIF, OCIF-CB	6.54e-05
20	113	100.0	399	20	R99942	Mutated OCIF, OCIF-CL	6.54e-05

LT 2 199951 standard; Protein; 84 AA. 189951; 23-APR-1997 (first entry)

RESULT

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6.54e-05 6.54e-05 6.54e-05 6.54e-05 6.54e-05 6.54e-05 6.54e-05 13.90e+01 1.66e+02 1.16e+02 1.16e+02 1.16e+02 1.16e+02 1.16e+02 1.16e+02 1.16e+02 1.16e+02 1.43e+02 1.43e+02 1.43e+02 1.43e+02	11.22 22.23 27.72 20.23 20.23
Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C3 Full length osteolas Bacillus thuringiensi 67-kD protein toxin. pCTD ORF 8. Platelet adhesion inh Thermostable beta-gal Spartle patched protein Thermostable beta-gal Bettle patched protein Rat allograft inflamm P. denitrificans COB D Chondrolinase AC. Acetybolyanine amido	Human ara Kb beta gal Osteoinductive retrov RNase T1. Malolactic enzyme fro Feline Immunodeficien FIV DUTCH19K1 envelop Composite sequence of
R899933 R999933 R8999334 R8999334 R899925 R899925 R899925 R899995 R88099 R88099 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R88095 R8800 R8800 R8800 R88005 R88005 R8800 R8800 R8800 R8800 R8800 R8800 R8800 R8	
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### ALIGNMENTS

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DNR encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 2; Page 67: 183pp; Japanese.

Claim 2; Page 67: 183pp; Japanese.

Claim 2; Page 67: 183pp; Japanese.

The sequences given in 189921-23 and 189926 represent fragments of the osteoclastogenesis inhibitory factor (OCIF) of the invention.

The OCIF has a molecular weight by SDS-PAGE of 60 kb under reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg.C, and is bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                                      22-ApR-1997 (first entry)
Osteoclastogenesis inhibitory factor N-terminal fragment.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 113; DB 20; Length 15;
Pred. No. 6.54e-05;
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                                                                                                                                                                 29-A0G-1996.
20-FEB-1996; JO0374.
20-FEB-1996; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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R99926 standard; peptide; 15 AA.
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Best Local Similarity 100.0%;
Matches 15; Conservative
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                                                                                                                                    Homo sapiens.
WO9626217-A1.
                                                                                                                osteoporosis
  RESULT
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osteoclastogenesis inhibitory factor (OCIF) of the IULI length sequence represents OCIF-OF in which amino acids 62-380 of the mature OCIF protein are replaced by Leuval. These changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Mutațed OCIF, OCIF-CPst.
Ostegclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Mutated OCIF, OCIF-CCR3.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                                                                                                                                                                                                                                                DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 89; Page 131; 183pp; Japanese.

This sequence represents a mutated version of the full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207500.
GOTO M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T; Nakaqawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H; N-PSDB; T33177.
                                                                                                                                                                                                                                                                  Morinaga T
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 113; DB 20; Length 84;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels
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21-UÜL-1995; JP-207508.
CSNWW DSNOW BRAND MILK PROD CO LTD.
GCOTO |M. Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33181.
                                                                        Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 15; Conservative
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/note= "Mature OCIF-CPst"
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                                                                                                        "Signal peptide"
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                                                        Synthetic.
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sequence represents OCIF-CCR3 in which amino acids 86-380 of the mature OCIF protein are deleted. The OCIF of the invention mature OCIF protein are deleted. The OCIF of the invention and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Claim 74; Page 124; 183pp; Japanese.
This sequence represents a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence represents OCIF-CCR4 in which amino acids 123-380 of the
mature OCIF protein are deleted. The OCIF of the invention
has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
and 120 kD under non-reducing conditions. The protein is adsorbed onto
cation-exchangers or heparin and its activity is lowered after 10 mins
at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
deg.C. OCIF is useful in the control of bone resorption and therefore
in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
                                                                                                                                                                                                              Score 113; DB 20; Length 106;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
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Pred. No. 6.54e-05;
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20-FEB-1996.
7 20-FEB-1995; JP-05497.
7 21-JUL-1995; JP-05497.
8 21-JUL-1995; JP-05497.
9 21-JUL-1995; JP-05497.
9 20-VIL-1995; JP-05497.
9 SNOW BRAND MILK PROD CO LTD.
GOTO M. Higashio K. Kobayashi F. Mochizuki S. Mc NRYAgawa N. Shima N. Tsuda E. Ueda M. Yano K. Ya NPESDB; T33176.
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22-APR-1997 (first entry)
Osteoclastogenesis inhibitory factor 5.
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R99946 standard; Protein; 143 AA.
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1997 (first entry) Mutated OCIF, OCIF-CCR4.
                                                                                                                                                                                                                                                    15; Conservative
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This sequence represents full length osteoclastogenesis inhibitory factor (OCIF) 4. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under norrequeing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 26; page 76-77; 183pp; Japaneses.

This sequence represents full length osteoclastogenesis inhibitory factor (OCIF) 5. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducting conditions and 120 kD under non-reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C. and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osteoclastogenesis inhibitory factor 4. Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
    Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ġoto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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                                                                     Location/Qualifiers
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Local Similarity 100.0%;
nes 15; Conservative
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n 22.154
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                                                                                                                                   Protein 22.145 /note= "Mature OCIF 5"
                                                                                              Peptide 1..21
/note= "Signal peptide"
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                                                       Homo sapiens.
                                    osteoporosis.
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Matches
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DNA encoding osteoclastogenesis inhibitory factor protein - useful DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 86; Page 130-131; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This osteoclastogenesis inhibitory factor (OCIF) of the invention. This control is confirmed are deleted. These changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCIF of invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and resorption, e.g. osteoporosis.

Sequence 187 AA;
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Mutated OCIF, OCIF-CBsp.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-07508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashi F, Mochizuki S, Morinaga T; Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H; N-PSDB; T33180
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useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                                                                             Length 154;
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                                                                                                                                             Score 113; DB 20; L
Pred. No. 6.54e-05;
0; Mismatches 0;
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Best Local Similarity 100.0%;
                                                                                                                                                                                                        15; Conservative
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                                                                                                 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoporosis.
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                                                                   osteoporosis
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20-FEB-1995; JP-054977.

R (20-FEB-1995; JP-054977.

R (20-FEB-1995; JP-054977.

R (20-FEB-1995; JP-054977.

R (20-FEB-1995; JP-054977.

R (20-M) | SNOW BRAND MILK PROD CO LTD.

GOLO M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;

Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;

NPH 196-402320440.

DR N-PSDB; T33174.

PT Calaim 68; Page 121-122; 183pp; Japanese.

C Claim 68; Page 121-122; 183pp; Japanese.

C Taim 68; Page 121-122; 183pp; Japanese.

C This Sequence represents a mutated version of the full length

CC Steoclastogenesis inhibitory factor (OCIF) of the invention.

CC Steoclastogenesis inhibitory factor (OCIF) of the invention.

CC sequence represents OCIF-CDD2 in which amino acids 252-380 of the

CC sequence represents OCIF-CDD2 in which amino acids 252-380 of the

CC sequence represents or repeating conditions.

CC ation exchangers or heparin and its activity is lowered after 10 mins

CC ation exchangers or heparin and its activity is lowered after 10 mins

CC ation exchangers or heparin and its activity is lowered after 10 mins

CC ation exchangers or heparin and its activity is lowered after 10 mins

CC ation or CC and mins at 56 deg.C, and is lost after 10 mins at 90

CC deg.C. OCIF is useful in the control of bone resorption and therefore
                                                                                                                                                                                                                                                                     DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 17. Page 123. Baspp. Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents offer-CDDI in which amino acids 177-380 of the mature COIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore osteoporosis.
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Mutated COIF, OCIF-CDD2.
OSteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoclastosis.
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                                                                                                                                                                                                    Morinaga I;
Yasuda H;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0
                                                                                                    20-FÉB-1996; J00374.
20-FÉB-1995; JP-05497.
21-JÚL-1995; JP-207508.
(SNOM ) SNOW BRAND MILK PROD CO LTD.
GOLO M. Higashio K, Kobayashi F, Mochizuki S, NAKAGAWA N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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Best Local Similarity 100.0%;
Matches 15; Conservative
             /note | Mature OCIF-CDD1"
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Protein 22.272
/note= "Mature OCIF-CDD2"
"Signal peptide"
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                                                          W09626217-A1.
29-AUG-1996.
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The properties of the control, esp. treatment of osteoporosis.

To bone resorption control, esp. treatment of osteoporosis.

Claim 83, Page 128-139; 183pp; Japanese.

Control osteoclastogenesis inhibitory factor (OCIF) of the full length of sequence represents a mutated version of the full length of costeoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CSph in which amino acids 298-380 of the mature ocif protein are replaced by Ser-Leu-Asp. These changes are caused by the introduction of a restriction site in the DNA encoding this protein.

The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                                                                                                                                                                                                                                                      23-APR-1997 (first entry)
Mutated OCIF, OCIF-CSph.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteopozosis.
in the treatment and prevention of disorders of bone resorption, e.g.
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Mutated OCIF, OCIF-DDD1.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
                                                                      Score 113; DB 20; Length 272;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0
                                                                                    Pred. No. 6.54e-05;
0; Mismatches 0; Indels
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21-JUL-1995; JP-207508.
(SNOW) NOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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R99949 standard; Protein; 321 AA.
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                                                                    Match 100.0%;
Local Similarity 100.0%;
les 15; Conservative
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                                     272 AA;
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WPI; 96-402320/40.
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                     osteoporosis
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                                      Sequence
                                                                  Query Match
Best Local S
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 59; Page 115-116; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DDD2 in which amino acids 253-326 of the mature oCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto
                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Market No. 1991, 1991, 1992, treatment of osteoprorosis for bone resorption control, esp. treatment of osteoprorosis for bone resorption control, esp. treatment of osteoprorosis for bone resorption control, appeares the sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DDD1 in which amino acids 178-252 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto extinon-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
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Yasuda H;
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Yasuda H;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-00L-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, NAKAGAWA N, Shima N, Tsuda E, Ueda M, Yano K, WPI: 96-402320/40.
                                                                                                                                                                                          20-FEB-1996; J00374.
20-FEB-1996; JP-054977.
21-JUL-1995; JP-054977.
SNOW ) SNOW BRAND MILK PROD CO LTD.
GCto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
Protein 22..326
/note= "Mature OCIF-DDD1"
/note= "Mature 198..199
/note= "Positition of deletion, delta 178-252"
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/note= "Signal peptide"
Protein 22..327
/note= "Mature COIF-DDD2"
Misc_difference 273..274
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Local Similarity 100.0%;
les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 AA;
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                                                                                                                                    WO9626217-A1.
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Matches
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In Four in the first protein of osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis for laim 65. Page 119-121; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CC in which amino acids 331-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 50 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Mutated OCIF, OCIF-DCR2.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
osteoporosis.
                                                                                                                                                                                                                                                                                                                                          Mutated OCIF, OCIF-CC. OSteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
                                                                                                                      Score 113; DB 20; Length 327;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels
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20-FEB-1995; JP-054977.
21-UTL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
NAKAGAWA N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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R99937 standard; Protein; 359 AA.
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Matches 15; Conservation
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Best Local Similarity 100.0%;
                                                                                                                        100.0%;
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                                                                                                                                                           15; Conservative
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/note= "Signal peptide"
Protein 22.351
/note= "Mature OCIF-CC"
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                                                                                                                                                                                                  NNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis for and 47. Page 107-109; 183pp; Japanese.

This sequence represents a mutated version of the full length osteogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR2 in which amino acids 43-84 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kB under reducing conditions and 120 kB under non-reducing conditions. The protein is adsorbed onto cation-exchanges or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of sorders of bone resorption, e.g.
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Mutațed OCIF, OCIF-DCR4.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR4 in which amino acids 123-164 of the mature OCIF protein are deleted. The OCIF of the invention
                                                                                                                                                                                                                                                                                                                                                                                                              Score 113; DB 20; Length 359;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0;
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Yasuda H;
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                                                                                                  20-FEB-1995; JR0374.
21-PEB-1995; JP-054977.
21-JÜL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GCto | M. Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PS-PB, T33167.
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-UTL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
Goto M. Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein 22.359
/note= "Mature OCIF-DCR4"
Misc_difference 143..144
/note= "Positition of deletion, delta 123-164"
                                               Miss_difference 63..64 /note= "Position of deletion, delta 43-84"
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les | 15; Conservative
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orote= "Mature OCIF-DCR2"
 1..21
"Signal peptide"
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/note= "Signal peptide"
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                                                                                       29-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
 Peptide
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Matches
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AC R9
DT 23
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has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR3 in which amino acids 85-122 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption and therefore in the control of disorders of bone resorption, e.g.
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
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22-APR-1997 (first entry)
Mature osteoclastogenesis inhibitory factor.
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/note= "Position of deletion, delta 85-122"
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW.) SNOW BRAND MILK PROD CO LTD.
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R99938 standard; Protein; 360 AA.
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les 15; Conservative
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Best Local Similarity 100.0%;
Matches 15; Conservative
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/note= "Mature OCIF-DCR3"
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/note= "Signal peptide"
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Best Local Similarity 100.0%;

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New human tumour necrosis factor receptor - used to develop prods.

Tor treating e.g. tumours, infection, auto:immune disease, graft rejection, cytotoxicity or inflammation

Sclaim 14. Fig 15 59pp; English.

The receptor binds to TNF, and in particular, TNF-beta.

The receptor may be used for screening for antagonists and agonists of the receptor may be used for screening for antagonists and agonists of the receptor may be used for liquids for the receptor. Such agonists may be used to inhibit the growth of tumours, to stimulate cellular differentiation, to mediate the immune response and anti-viral response, to regulate growth and provide resistance to certain infections. The antagonists may be used therapeutically, to treat autoimmune diseases, inflammation, septic shock, to inhibit graft.

Sequence 390 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 6; Page 62-64; 183pp; Japaneses.

This sequence represents the mature osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE Of 60 kb under reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C., and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1997 (first entry)
Human tumour necrosis factor receptor.
Tumour necrosis factor TNF; receptor; TNF-beta; ligand; tumour:
differentiation; immune response; autoimmune disease; inflammation; septic shock; graft-versus-host; apoptosis.
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                                                                                                                                                                                                                                                                                                         Morinaga T;
Yasuda H;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels
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                                                                                                                                                            20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-20508.
(SNOW BRAND MILK PROD CO LTD.
GCto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T36685.
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R99357 standard; Protein; 390 AA.
R99357;
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15-MAR-1995; U03216.
15-MAR-1995; W0-U03216.
29-MAR-1995; ZA-002587.
(HUMA-) HUMAN GENOME SCI INC.
Fleischmann RD, Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative
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W09628546-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AA;
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                                   osteoporosis.
                                                                      Homo sapiens.
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                                                                                                                                   29-AUG-1996.
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 80; Page 126-128; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CBst in which Gln 371 is substituted by the ness of the material of the material of the material of the material of the material of the material of the material of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or reparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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23-ARR-1997 (first entry)
Mutated OCIF, OCIF-CL.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
SNOW BRAND MILK PROD CO LTD.
GGto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33178.
Pred. No. 6.54e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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R99942 standard; Protein; 399 AA.
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R99948 standard; Protein; 393 AA.
R99948;
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/note= "Mature OCIF-CBst"
Misc_difference 392
/label= Gln771eu
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                               23-APR-1997 (first entry)
                                                       15; Conservative
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Protein 22.399
/note= "Mature OCIF-CL"
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                                                       Matches
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Claim 62. Page 117-119; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CL in which amino acids 379-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption of incomment and prevention of disorders of bone resorption, e.g.
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No. A benceding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis

for bone resorption control, esp. treatment of osteoporosis

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents offr-C21s in which the 21st Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has all molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Osteoplastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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0
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Yasuda H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 113; DB 20; Length 399;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels
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                                                                                                                                      Goto M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-701995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
Goto M. Higashio K, Kobayashi F, Mochizuki S, Wakagawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSDB; Ţ33163.
                                                20-FB-1996; JO0374.
20-FB-1995; JF-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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Matches 15; Conservative
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/note= "Mature OCIF-C21s"
Misc_difference 277
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/note= "Signal peptide"
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W09626217-A1.
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C20S in which the 20th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and tharefore in the control of bone resorption of circum.
                                                                                                                                                                                                                                                                                                                                                                                           Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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                                                                      Length 401;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
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                                                                 Score 113; DB 20; Length 401
Pred. No. 6.54e-05;
0; Mismatches 0; Indels
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21-FEB-1996; JP-054977.
21-JUL-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW DRAND MILK PROD CO ITD.
GCto M, Higashio K, Kobayashi F, Mochizuki S,
Nakaqawa N, Shima N, Tsuda E, Ueda M, Yano K,
NPI: 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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nes 15; Conservative
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22-APR-1997 (first entry)
Mutated OCIF, OCIF-C20S.
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'note= "Mature OCIF-C20S"
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/note= "Signal peptide"
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                                                                                                                                                                                                               1 ETFPPKYLHYDEETS 15
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                      401 AA;
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WO9626217-A1.
29-AUG-1996.
osteoporosis
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Matches
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 41. Page 103-105, 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C238 in which the 21rd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is absorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF 1s useful in the control of bone resorption and therefore
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents offr-C22s in which the 22nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in the treatment and prevention of disorders of bone resorption, e.g.
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Yasuda H;
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 113; DB 20; Length 401;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
                                                                                                                             W0962041.
29-AUG-1996.
29-AUG-1996.
R 20-FEB-1995; JP-054977.
PR 21-JUL-1995; JP-207508.
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
T GOLD M, Higashio K, Kobayashi F, Mochizuki S, Moranda M, Tsuda E, Ueda M, Yano K, Yana N, Shima N, Tsuda E, Ueda M, Yano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Shima N, Tsuda E, Ueda M, Tano K, Yana N, Shima N, Shima N, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda M, Tsuda E, Ueda E, Ueda E, Ueda E, Ueda E, Ueda E, Ueda E, Ueda E, Ueda E,
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
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22..401
/note= "Mature OCIF-C23S"
Misc_difference 400
/label= C23S
W0965c--
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22-APR-1997 (first entry)
Mutated OCIF, OCIF-C22S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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"Mature OCIF-C22S"
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Nakagawa N, Shima N,
WPI; 96-402320/40
N-PSDB; T33164.
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cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. at 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OoIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Full length osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutated OCIF, OCIF-C195.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
                                                                                                                                                                               Score 113; DB 20; Length 401;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 113; DB 20; Length 401; Pred. No. 6.54e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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20-FEB-1996; JO0374.
20-FEB-1996; JP-054977.
21-UT-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashi F, Mochizuki S,
Nakaqawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33161.
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Matches 15; Conservative
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/note= "Mature OCIF-C195"
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/note= "Signal peptide"
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Homo sapiens.

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W0962617-A1.

29-A¢G-1996.

29-A¢G-1996.

20-A¢G-1996.

20-EpB-1995; JP-054977.

PF 20-EpB-1995; JP-054977.

PF 21-J¢L-1995; JP-054977.

PF 21-J¢L-1995; JP-054977.

PF 21-J¢L-1995; JP-207508.

PF 21-J¢L-1995; JP-207508.

PF 20-EpB-1995; JP-207508.

PF 20-EpB-1995; JP-207508.

PF 20-EpB-1995; JP-207508.

PF 30-EpB-1995; 
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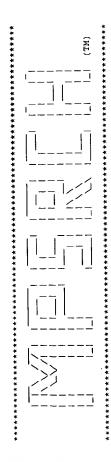
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0;
                             Location/Qualifiers
                                                                                                                   Protéin 22..401
/note= "Mature OCIF, claim 6"
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Best Local Similarity 100.0%;
Matches 15; Conservative
                                                        ".Signal peptide"
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Search completed: Wed Dec 3 10:07:20 1997 Job time 6 secs.



Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Dec 2 14:52:31 1997; MasPar time 2.86 Seconds 151.367 Million cell updates/sec pular output not generated.

Run on:

>US-08-915-004-7 (1-15) from US08915004.pep 113 1 ETFPPKYLHYDEETS 15 Description: Perfect Score: Sequence: itle:

Scoring table:

91006 seqs, 28888923 residues PAM 150 Gap 15 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:ani 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev pir51 Database:

Mean 26.254; Variance 43.975; scale 0.597 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Pred. No.	3.59e-01	7.73e-01	2.38e+00	2.38e+00	4.95e+00	4.95e+00	1.01e+01	1.01e+01	2.05e+01	2.05e+01	2.05e+01	2.05e+01	2.05e+01	2.05e+01	2.89e+01	2.89e+01	2.89e+01	2.89e+01	2.89e+01	2.89e+01	2.89e+01
	Description	probable membrane pr	histidine decarboxyl	beta-fructofuranosid	beta-fructofuranosid	MHC class I protein	cytochrome-c oxidase	hypothetical protein	72K crystal protein	hypothetical protein	hypothetical protein	hypothetical protein	cytochrome-c oxidase		probable membrane pr	farnesyl-pyrophospha	ribulose-bisphosphat	malate oxireductase	acetylcholinesterase	acetylcholinesterase	probable amino acid	arylphorin precursor
	ID	S53409	549218	S61503	J00991	I50036	\$26034	S67612	A43647	S01180	507880	H37386	526022	540822	S55151	A35726	JC2307	544330	ACRYE	A38868	S54032	JQ1045
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RESULT

ORGANISM

DATE

849218 #type complete
histidine decarboxylase (EC 4.1.1.22) - Vibrio anguillarum
histidane Vibrio anguillarum
16-Feb-1995 #sequence_revision 12-May-1995 #text_change
22-Nov-1996

S60898; S49218 S60898 Tolmasky, M.E.; Actis, L.A.; Crosa, J.H.

#authors ACCESSIONS REFERENCE

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Plant J. (1993) 4:545-554
Molecular characterization of the gene for carrot cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sturm, A.; Chrispeels, M.J.
Plant Cell (1990) 2:1107-1119
cDNA cloning of carrot extracellular beta-fructosidase and
its expression in response to wounding and bacterial
                                                                                                                                                    carbon-carbon lyase; carboxy-lyase; pyridoxal phosphate
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beta-fructosidase; vacuolar invertase
                                                                                                                                                                                     Gaps
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#formal_name Daucus carota #common_name carrot
27.0ct-1996 #sequence_revision 27.0ct-1996 #text_change
              A histidine decarboxylase gene encoded by the Vibrio anguillarum plasmid pJM1 is essential for virulence histamine is a precursor in the biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change
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##cross-references GB:M58362
FICATION #superfamily beta-fructofuranosidase
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Pred. No. 7.73e-01;
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    Mol. Microbiol. (1995) 15:87-95
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8; Conservative
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Best Local Similarity 61.5%;
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                                                                                                                     Gaps
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Immunogenetics (1992) 36:166-174
Reptilian class I major histocompatibility complex genes
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                                                                                                                                                                                                                                                                                                         MHC class I protein - axolotl (fragment)
#formal_name Ambystoma mexicanum #common_name axolotl
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
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hydrolase
#molecular-weight 66813 #checksum 3928
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##residues
1-37 ##label GRO
##cross-references GB:M81089; NID:g210935; CDS_PID:g555414
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                                                        Score 62; DB 5; Deny Dred, No. 2.38e+00;
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Pred. No. 4.95e+00;
1; Mismatches 1; Indels
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Genetics (1992) 130:471-498
The mitochondrial genomes of
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                                                                 Query Match 54.9%;
Best Local Similarity 61.5%;
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Local Similarity 77.8%;
hes 7; Conservative
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  glycosidase;
#length 592
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J. Bacteriol. (1988) 170:4732-4738
Molecular characterization of a gene encoding a 72-kilodalton
mosquito-toxic crystal protein from Bacillus thuringiensis
subsp. israelensis.
A43647
                                                                                                                                                                                                                                                #domain cytochrome-c oxidase chain I homology #label COI
#length 525 #molecular-weight 58463 #checksum 9978
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                                                                                                                                    *superfamily cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology copper binding; electron transfer; heme; membrane-associated
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03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
               the authors translated the initiation codon ATT for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein D2476
#formal_name Saccharomyces cerevisiae
|12.Jul-1996 #sequence_revision 12-Jul-1996 #text_change
| 12-Jul-1996
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MARY #length 294 #molecular-weight 33811 #checksum 9485
                                                                                                                                                                                               complex; mitochondrion; oxidative phosphorylation;
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72K crystal protein - Bacillus thuringiensis subsp.
israelensis
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hypothetical protein YDL076c - yeast (Saccharomyces
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Pred. No. 1.01e+01;
4; Mismatches 2; Indels
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larity 60.0%; Pred. No. 4.95e+00;
Conservative 1; Mismatches 3; Indels
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Matches 5; Conservative
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hypothetical protein 1 - Methanobacterium thermoautotrophicum
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                                                             #authors Adams, L.F.; Visick, J.E.; Whiteley, H.R.
#journal J. Bacteriol. (1989) 717:521-530
#title A 20-kilodalton protein is required for efficient production of the Bacillus thuringiensis subsp. israelensis 27-kilodalton crystal protein in Escherichia coll.
#cross-references MUID:89123065
#accession A3226
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Mucleic Acids Res. (1988) 16:4053-4067
Analysis of the entire nucleotide sequence of the cryptic plasmid of Chlamydia trachomatis serovar Ll. Evidence for
                                                                                                                                                                                                                                preliminary; not compared with conceptual translation
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hypothetical protein N-1 - Chlamydia trachomatis plasmid
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07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
18-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
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#length 203 #molecular-weight 23076 #checksum 8385
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#length 643 #molecular-weight 72348 #checksum 6237
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Nucleic Acids Res. (1990) 18:363
Complete nucleotide sequence of plasmid pME2001 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    involvement in DNA replication.
#cross-references MUID:88233998
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##residues 566-643 ##label ADA
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##residues 1-643 ##label DON ##cross-references GB:M31737
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Local Similarity 41.7%;
hes 5; Conservative
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Best Local Similarity 70.0%;
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2 TFPPKYLHYDEE 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Comanducci, M.; Ricci, S.; Ratti, G.
#journal Mol. Microbiol. (1988) 2:531-538
#title The structure of a plasmid of Chlamydia trachomatis believed
to be required for growth within mammalian cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Comanducci, M.; Ricci, S.; Cevenini, R.; Ratti, G. Plasmid (1990) 23:149-154
Diversity of the Chlamydia trachomatis common plasmid in biovars with different pathogenicity.
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                    #formal_name Chlamydia trachomatis
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
01-Dec-1995
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                                                                                 #length 273 #molecular-weight 30744 #checksum 8715
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                                                                                                             y Match 49.6%; Score 56; DB 10; Length 273; Local Similarity 58.3%; Pred. No. 2.05e+01; nes 7; Conservative 2; Mismatches 3; Indels
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Pred. No. 2.05e+01;
5; Mismatches 2; Indels
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CE | $01920
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##regidues 1-330 ##label COM2
##cross-references EMBL:X07547
               1-273 ##label BOK
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                                 ##cross-references EMBL:X17205
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Best Local Similarity 41.7%;
Matches 5; Conservative
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##molecule_type DNA
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S26022 #type complete cytochrome-c oxidase (EC 1.9.3.1) chain I - pig roundworm

S26022

RESULT

TITLE

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#domain cytochrome-c oxidase chain I homology #label CO1
#length 525 #molecular-weight 58529 #checksum 1290
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Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oxidase chain I homology copper binding; electron transfer; heme; membrane-associated complex; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein
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##note the nucleotide sequence was submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                      two nematodes, Caenorhabditis
                                                                                                                                                                                                   Okimoto, R.; Macfarlane, J.L.; Clary, D.O.; Wolstenholme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okimoto, R.; Macfarlane, J.L.; Wolstenholme, D.R. Nucleic Acids Res. (1990) 18:6113-6118 Evidence for the frequent use of TTG as the translation initiation codon of mitochondrial protein genes in the nematodes, Ascaris suum and Caenorhabditis elegans.
                        #formal_name mitochondrion Ascaris suum #common_name pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the authors translated the initiation codon ATT for residue 1 as 1le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references EMBL:X54253
##note the authors translated the initiation codon ATT for
residue 1 as 11e
                                                    roundworm
12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change
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hypothetical protein f678 - Escherichia coli
#formal_name Escherichia coli
19-May-1994 #sequence_revision 01-Sep-1995 #text_change
01.Sep-1995
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translation not shown
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Query Match

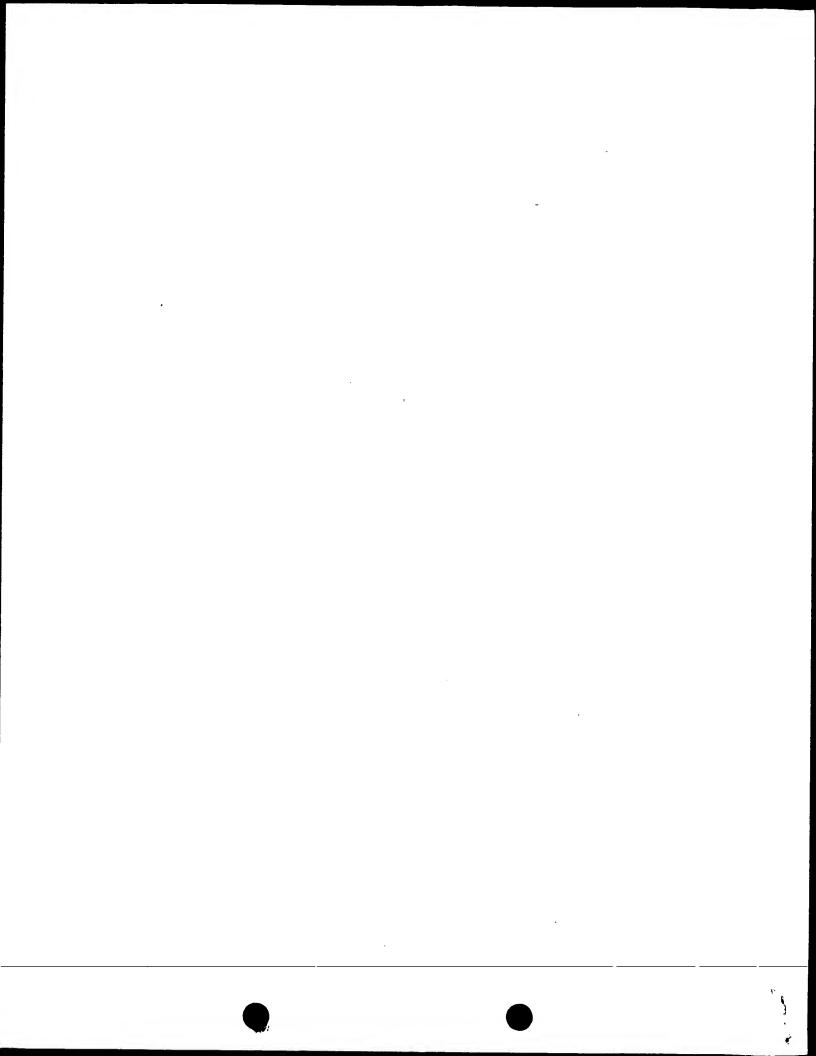
Best Local Similarity 50.0%; Pred. No. 2.05e+01;

Matches 5; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                          #journal Genetics (1992) 130:471-498
#title The mitochondrial genomes of elegans and Ascaris suum.
#cross references MUID:92201635
                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
##residues 1-525 ##label OKI
##cross-references EMBL:X54253
mitochondrion (SGC4)
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##residues 1-25 ##label OK2
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Mallet, L.; Bussereau, F.; Jacquet, M.
Yeast (1995) 11:1195-1209
A 43:5 kb segment of yeast chromosome XIV, which contains
MFA2, MEP2, CAP/SRV2, NAM9, FKBI/FPRI/RBP1, MOM22 and CPT1,
predicts an adenosine deaminase gene and 14 new open
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Library, November 1994
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                                                                                                                                                                                                                                                                                                               hypothetical protein JTA1056; hypothetical protein N1216;
                                                                                                                                                                                                                                                                      probable membrane protein YNL132w - yeast (Saccharomyces
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#formal_name Saccharomyces cerevisiae
08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
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                                                                                                Gaps
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submitted to the Protein Sequence Database, April 1996
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farnesyl-pyrophosphate synthetase - human
prenyltransferase and farnesyl-diphosphate synthase
dimethylallyltranstransferase (EC 2.5.1.1);
                #length 678 #molecular-weight 77248 #checksum 649
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Pred. No. 2.05e+01;
0; Mismatches 1; Indels (
                                                     Score 56; DB 9; Length 678; Pred. No. 2.05e+01;
                                                                                                1; Indels
                                                                                                5; Mismatches
Library, October 1993
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##residues 1-1056 ##label MAW
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Local Similarity 85.7%;
                                                       Query Match
Best Local Similarity 40.0%;
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Sheares, B.T.; White, S.S.; Molowa, D.T.; Chan, K.; Ding, V.D.H.; Kroon, P.A.; Bostedor, R.G.; Karkas, J.D. Biochemistry, (1989) 288:8129-8135 Cloning, analysis, and bacterial expression of human farnesyl pyrophosphate synthetase and its regulation in Hep G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catalyzes the condensation of isopentenyl diphosphate with dimethylallyl diphosphate forming geranyl diphosphate and pyrophosphate; catalyzes the condensation of isopentenyl diphosphate with geranyl diphosphate forming farnesyl diphosphate and pyrophosphate forming farnesyl steroidogenesis, lipoprotein synthesis #superfamily farnesyl-pyrophosphate synthetase cholesterol biosynthesis; homodimer; transferase #length 353 #molecular-weight 40520 #checksum 7314
                                                                                                                                                                                                                                                         farnesyl pyrophosphate synthetase, 3-hydroxy-3-methylglutaryl coenzyme A reductase, and 3-hydroxy-3-methylglutaryl coenzyme A synthase by phorbol
                                                                                                                                                           Wilkin, D.J.; Kutsunai, S.Y.; Edwards, P.A.
J. Biol. Chem. (1990) 265:4607-4614
Isolation and sequence the human farnesyl pyrophosphate
synthetase cDNA. Coordinate regulation of the mRNAs for
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geranyltranstransferase (EC 2.5.1.10)
#formal_name Homo sapiens #common_name man
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
06-Sep-1996
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Pred. No. 2.89e+01;
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##residues 8-115,'I',117-353 ##label SHE
##cross-references GB:M29863
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##cross references GB:J05262
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Best Local Similarity 33.38;
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:52:04 1997; MasPar time 2.01 Seconds 158.672 Million cell updates/sec Run on:

>US-08-915-004-7 (1-15) from US08915004.pep 113 1 ETFPPKYLHYDEETS 15 plar output not generated. Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

59021 seqs, 21210388 residues

Searched:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 27.188; Variance 37.530; scale 0.724 Statistics:

## SUMMARIES

		P					
Result No.	Score	Query Match	Query Match Length	DB	ID	Description	Pred. No.
	62	54.9	592	5	INVA_DAUCA	BETA-FRUCTOFURANOSIDA	4.87e-01
2	9	53.1	252	σ	TRY I DROME	TRYPSIN IOTA PRECURSO	1.15e+00
m	9	53.1	423	11	YPIA_BACSU	HYPOTHETICAL 48.3 KD	1.15e+00
4	9	53.1	525		COX1_CAEEL	CYTOCHROME C OXIDASE	1.15e+00
S	59	52.2	1188	m	DPOL_ADE40	DNA POLYMERASE (EC 2.	1.75e+00
9	58	51.3	643	~	CR72_BACTI	72 KD CRYSTAL PROTEIN	2.65e+00
7	56	49.6	273	Ξ	YP30_METTH	HYPOTHETICAL 30.7 KD	6.01e+00
80	56	49.6	332	4	GP8D_CHLTR	VIRULENCE PROTEIN PGP	6.01e+00
σ	56	49.6	458	œ	RBL2_RHOCA	RIBULOSE BISPHOSPHATE	6.01e+00
10	26	49.6	510	11	YQBA_BACSU	HYPOTHETICAL 58.5 KD	6.01e+00
11	56	49.6	525	7	COX1_ASCSU	CYTOCHROME C OXIDASE	6.01e+00
. 12	56	49.6	678	Π	YIHO_ECOLI	HYPOTHETICAL 77.2 KD	6.01e+00
13	56	49.6	804	œ	RIR1_HSV6U	RIBONUCLEOSIDE-DIPHOS	6.01e+00
14	56	49.6	1056	Ξ	YNN2 YEAST	HYPOTHETICAL 119.3 KD	6.01e+00
15	55	48.7	353		FPPS_HUMAN	FARNESYL PYROPHOSPHAT	8.97e+00
16	55	48.7	565	9	MAOX_SCHPO	MALATE OXIDOREDUCTASE	8.97e+00
17	55	48.7	586	-	ACES_TORCA	ACETYLCHOLINESTERASE	8.97e+00
18	55	48.7	590	П	ACES TORMA	ACETYLCHOLINESTERASE	8.97e+00
19	S	48.7	604	7	PAP1_YEAST	PUTATIVE AMINO-ACID P	8.97e+00
20	55	48.7	759	-	ARY1_CALVI	ARYLPHORIN A4 PRECURS	8.97e+00
21	54	47.8	154	m	ELYS_HALWA	EGG-LYSIN PRECURSOR (	1.33e+01
22	54	47.8	154	m	ELYS_HALSO	EGG-LYSIN PRECURSOR (	1.33e+01

1.33e+01	1.33e+01	1.33e+01	1.33e+01	1.33e+01	1.33e+01	1.33e+01	1.33e+01	1.33e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	ω.	2.89e+01	83	2.89e+01	O1	2.89e+01
EGG-LYSIN PRECURSOR (	EGG-LYSIN PRECURSOR (	PUTATIVE TRANSCRIPTIO	RIBULOSE BISPHOSPHATE	RIBULOSE BISPHOSPHATE	IRON-REGULATED OUTER	SUCROSE SYNTHASE (EC	HYPOTHETICAL 117.0 KD	HYPOTHETICAL 130.8 KD	PROTEIN A52.	PROTEIN A52.	CAPSULE POLYSACCHARID	PROBABLE 6-PHOSPHO-BE	BETA-GALACTOSIDASE (E	BETA-GALACTOSIDASE (E	BETA-GALACTOSIDASE (E	LEU/VAL/ILE AMINO-ACI	HYPOTHETICAL PROTEIN	HYPOTHETICAL OXIDORED	PUTATIVE SERINE CARBO	HYPOTHETICAL PROTEIN	HYPOTHETICAL 92.1 KD	BOTULINUM NEUROTOXIN
ELYS_HALRU	ELYS_HALCO	TFS2_CAEEL	RBL2_RHOSH	RBL2_RHORU	IRGA_VIBCH	SUSY_ALNGL	YG35_YEAST	YMV2_CAEEL	VA52_VACCC	VA52_VACCV	LIPA_NEIME	GLVG_BACSU	BGAL_SULSH	BGAM_SULSO	BGAL_SULSO	BAP2_YEAST	Y006_MYCGE	YIV6_YEAST	YSS2_CAEEL	Y241 MYCGE	YA73_SCHPO	вхЕ_сгово
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23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

				PRECURSOR (EC 3.2.1.26)			DICOTYLEDONEAE; APIALES;												PHLOEM UNLOADING AND IN		CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-	URANOSIDES.	E CELL WALL.	TO WOUNDING AND BACTERIAL INFECTION.	SIMILARITY: BELONGS TO FAMILE 32 OF GLICOSIL HIDROLASES. HUMBE NEE NE FENCH HUBEE ICOTVMPC OF BETA-FRICHOFIBANOSIDARE IN					1	; ZYMOGEN; SIGNAL.			IDASE, INSOLUBLE			Z		. Z	GLYCAN.	
	592 AA.		UPDATE)				ANGIOSPERMAE; D			SEQUENCE.							STURM A.;		ROLE IN		OF TERMINAL	FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES	SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL	ING AND BACT	Z OF GLICOSI FC OF BFTA-F	TWO SOLUBLE.				32.	GLYCOPROTEIN; CELL WALL;	39 (POTENTIAL).	(POTENTIAL).	BETA-FRUCTOFURANOSIDASE,	YME.		COMPLEX-TYPE GLYCAN		COMPLEX-TYPE GLYCAN	HIGH-MANNOSE-TYPE GLYCAN	IAL.
	PRT;		LAST SEQUENCE UPDATE)	INSOLUBLE ISOENZYME						ΑΓ	LACE;		, ,				EN S.,		N IMPORTANT		HYDROLYSIS	IDUES IN BE	IONICALLY	ISE TO WOUND	TO FAMILY 3	AND TWO S	  -  -			GLYCOSYL_HYDROL_F32.	GLYCOPROTEI		OR 40	BETA-F	ISOENZYME	BY SIM	COMPLE	POTENTIAL.	COMPLE	HIGH-W	POTENTIAL
	STANDARD;	23,	23,	SIDASE,	ATE HYD	RROT).	1; EMBRY			AND	NNE'S	). 11. 0 17. 1	A., CERISPEELS M.O.;	1)/111	,	: .:	, KNUDSEN	54 (1993)	PLAY AN	NSE.	LIVITY:	SIDE RES	COCATION	INDUCTION: IN RESPONSE	TELCINGS	THERE ARE ALLEASI LAREE I CARROT: ONE INSOLUBLE AND	57551; -		991.		GLYCOSIDASE;	31	48	292		74	170	195	311	348	570
			2 (REL.	OFURANC	-PHOSPE	OTA (CA	PLANT	AE.		ROM N.	OUEEN	3005650.	CHRIST	011.3	ROM N. 2	94035200.	RENZ K	:545-55	FUNCTION: MAY	STRESS RESPONSE.	TIC ACT	FURANO	LULAR	ION:	KLTY: L	ARE AL	62; G1	121; G10	1; 300	60900s		<b>,</b>	32	49		74	170	195	311	348	220
	INVA_DAUCA P26792;	01-AUG-199	01-AUG-1992	BETA-FRUCTOFURANOSIDASE,	(SUCROSE-6	DAUCUS CAROTA (CARROT)	EUKARYOTA; PLANTA; EMBRYOPHYTA;	UMBELLIFERAE	[1]	SEQUENCE FROM N.A.,	STRAIN-CV.		DIAME AL.	[2]	FINGE	MEDLINE: 9	RAMLOCH-LO	PLANT J. 4:545-554(1993)	-!- FUNCTI	STRESS	-!- CATALY	FRUCTO	i	-i- INDUCT	ALIMILA GUUMBER	CARROT	EMBL; M58362; G167551;	EMBL; X69321; G18324;	PIR; JQ099	PROSITE; PS00609;	HYDROLASE;	SIGNAL	PROPEP	CHAIN		ACT_SITE	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD
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COX1_CAEEL
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BY SIMILARITY.

REQUIRED FOR SPECIFICITY (BY SIMILARITY).

CE103ACF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAO L, WANG S., HICKEY D.A.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYITC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-|-XAA, LYS-|-XAA.
-!- SÜBCELLULAR LOCATION: EXTRACELLULAR.
-!- SÜBLELULARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOROKİN A.V., AZEVEDO V., ZUMSTEIN E., GALLERON N., EHRLICH S.D.,
SERROR P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; | U41476; G1134972; -.
FLYBAŞE; FBGN0015001; TRY-IOTA.
HYDROĻASE; SERINE PROTEASE; ZYWOGEN; SIGNAL; MULTIGENE FAMILY
                                                                         Score 62; DB 5; Length 592;
Pred. No. 4.87e-01;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
133 R -> W (IN REF. 2).
487 A -> V (IN REF. 2).
66813 MW; D41B4A3C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
ACTIVATION PEPTIDE.
TRYPSIN GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 9; LA
Pred. No. 1.15e+00;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                 01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TRYPSIN IOTA PRECURSOR (EC 3.4.21.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHERICAL 48.3 KD PROTEIN IN GCRA 5'REGION
                                                                                                                                                                                                                                                                     PRT; 252 AA
                                                                                                                                                                                                                                                                                                                                                                                                    DROSOPHILA MELANOGASTER (FRUIT FLY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26612 MW;
                                                                             54.9%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.1%;
ilarity 54.5%;
Conservative
                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L47709; G1146224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252
68
113
206
                                                                                                                                                    435 epfdpkwleydae 447
                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=168 / MARBURG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 eqfdsrflhyd 113
                                     592 AA;
                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | :::||||
ETFPPKYLHYD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=OREGON-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                   TRYI_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPIA_BACSU
P54389;
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
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                                     SEQUENCE
                                                                             Query Match
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ID YP
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GENETICS 130:471-498(1992).

-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CATALYTIC SUBUNIT OF THE BNYTHE ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME AS
AND COPPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INDER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.
-1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY. EMBL. X54252; G515883; -...
PIR: S26034; S26034.
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
                                                                                                                                           ;
0
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0
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OXIDOREDUCTASE; HEME; COPPER; MITOCHONDRION; TRANSMEMBRANE;
                                                                                           Score 60; DB 11; Length 423; Pred. No. 1.15e+00;
                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
IRON (HEME A3) (PROBABLE).
IRON (HEME A) (PROBABLE).
MW; FBD63AAD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESPIRATORY CHAIN; INNER MEMBRANE.

METAL 69 69 IRON (HEME A) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                               01-MAR'1992 (REL. 21, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.15e+00;
                                           423 AA; 48321 MW; 708A0553 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 5
DPOL_ADE40
BY 84311;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DNA POLYMERASE (EC 2.7.7.7).
                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                             525 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60;
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58463 MW;
                                                                                           53.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 60.0%;
les 6; Conservative
                                                                                                                                           Conservative
SUBTILIST; BG11496; YPIA. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                    361 qsfeaaylhyred 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
297
298
383
385
                                                                                                                                                                                                                               1 ETFPPKYLHYDEE 13
                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
297
298
298
383
385
525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443 fprkyldypd 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 FPPKYLHYDE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92201635
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[1]
SEQUENCE FROM N.A.
                     STRAIN-MARBURG;
                                                                                                                                                                                                                                                                                                                               CHLAMYDIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                       BACILLUS THURINGIENSIS (SUBSP. ISRAELENSIS).
PROKARYOTA, FIRMICUTES, ENDOSPORE-FORMING RODS AND COCCI, BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                           DONOVAN W.P., DANKOCSIK C., GILBERT M.P.;
J. BACTERIOL. 170:4732-4738(1988).
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPITHELIAL CELLS OF MOSQUITOS.
--- TOXIC SEGNENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
--- DEVELOPMENTAL STAGE: THE CRISTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
                      VIRIDAE; DS-DNA NONENVELOPED VIRUSES; ADENOVIRIDAE; MASTADENOVIRUSES
                                                                                                                                                                                                             Gaps
                                                               MEDLINE; 94087748.

DAVISON A.J., TELFORD E.A., WATSON M.S., MCBRIDE K., MAUTNER V.;
J. MOL. BIOL. 234:1308-1316(1993).

-!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
N PYROPHOSPHATE + DNA(N).
                                                                                                                                                                                                                                                                                                                          01-WAY-1991 (REL. 18, CREATED)
01-WAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
01-WAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
72 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58; DB 2; Length 643;
Pred. No. 2.65e+00;
2; Mismatches 1; Indels
                                                                                                                     -1- THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER.
-1- SIMILARITY: BELONGS TO FAMILY B OF DNA POLYMERASES.
BRBL; L19443; G303975; -2
DNA-DIRECTED DNA POLYMERASE; DNA REPLICATION: DNA-BINDING.
SEQUENCE 1188 AA; 135289 MW; C8EE6098 CRC32;
                                                                                                                                                                                     Score 59; DB 3; Length 1188; Pred. No. 1.75e+00; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLASMID PME2001.
ARCHAEBACTERIA: EURYARCHAEOTA: METHANOBACTERIALES;
METHANOBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      643 AA; 72348 MW; 0C528C2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
HYPOTHETICAL 30.7 KD PROTEIN.
                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                     643 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHANOBACTERIUM THERMOAUTOTROPHICUM
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (REL. 14, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.3%;
70.0%;
                                                                                                                                                                                        y Match
Local Similarity 60.0%;
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF THE SPORE COAT.
EMBL; M31737; G142763; -.
PIR; A43647; A43647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                       STANDARD;
                HUMAN ADENOVIRUS TYPE 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 tippnylayd 422
                                                                                                                                                                                                                                     377 fspdyltyee 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOXIN; SPORULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TEPPKYLHYD 11
                                                                                                                                                                                                                                                          3 FPPKYLHYDE 12
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       89008093
                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YP30_METTH
P14932;
                                                            STRAIN-DUGAN
                                                                                                                                                                                                                                                                                                      CR72_BACTI
P21256;
                                                                                                                                                                                                                                                                                                                                                                       PROTOXIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHLAMYDIA TRACHOMATIS.
LAISMID PLGV440, AND PLASMID PCHLI.
PRORARYOTA; GRACLLICUTES; SCOTOBACTERIA; RICKETTSIAS; CHLAMYDIALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGSNIA -> MALI (IN REF. 1 AND 4).
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                         / Match 19.6%; Score 56; DB 11; Length 273; Local Similarity 58.3%; Pred. No. 6.01e+00; St. Conservative 2; Mismatches 3; Indels les
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
PLASMID=POHLI; STRAIN=TRACHOMA SEROIYPE D;
MEDLINE; 90301796.
COMANDOCCI M., RICCI S., CEVENINI R., RATII G.;
PLASMID 23:149-154(1990).
1- PGP8-D IS REQUIRED FOR GROWTH WITHIN MAMMALIAN CELLS.
EMBL, X07547; 640731; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB 4; Length 332;
Pred. No. 6.01e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (APR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GP8D_CHLTR STANDARD; PRT; 332 AA.
P08788; P10554;
01-NOV-1988 (REL. 09, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
VIRULENCE PROTEIN PGP8-D (ORF8) (PROTEIN N-1/N-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1DEBSF46 CRC32;
MEDLINE; 90221821.
BOKRANZ M., KELETA A., MEILE L.;
BOCKERAZ M. STERN S., MEILE L.;
EMBL, X17205; 645718; -.
PIR; S07880: S07880.
PROTHETICAL PROTEIN: PLASMID.
SEQUENCE Z73 AA; 30744 MW; FF211F2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
PLASMID-PLGY40; STRAIN-L1/440/LN;
MEDLIN: 8823398.
HATI C., WARD M.E., CLARKE I.N.;
NUCLEIC ACIDS RES. 16:4053-4067(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
PLASMID-PLGV440; STRAIN-L2;
MEDLINE; 89013892;
COMANDUCCI M., RICCI S., RAITI G.;
MOL. MICROBIOL. 2:531-538(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS TO C-TERMINUS.
PLASMID-PLGV440; STRAIN-L1/440/LN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 AA; 37918 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.6%;
Local Similarity 41.7%;
hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X06707; G473191; --
EMBL; X06707; G473191; --
EMBL; J03321; G455146; --
PIR; S01180; S01180.
PIR; S01181; S01181.
PIR; S01920; S01920.
PIR; H37386; H37386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 typqkfmhflqe 236
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                                                                                                                                                                                                                                                                                                     223 spkylfyasetg 234
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LARIMER F.W., LU T.Y.S., BULEY D.M.;
SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE I, S-BISPHONERATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRACMENTATION OF THE PENTOSE SUBSTRAIE IN THE PHOTORESPIRATION PROCESS. BOTH RECTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: DEBLLOSE 1,5-BISPHOSPHATE + 0(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
-!- SPBUNIT: IN CONTRAST TO FORM I GENES, THE FORM II RUBISCO ARE COMPOSED OF ONLY LARGE SUBUNITS (BY SIMILARITY).
-!- THIS PROTEIN IS ENCODED WITHIN THE FORM II RIBULOSE-BISPHOSPHATE CARBOXYLASE OPERON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-168 / JH642;
KOBAYAȘHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO S., SATO T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYASE OXIDOREDUCTASE; MONOOXYGENASE; MÚLTIGENE FAMILY.

ACT_SÍTE 191 191

BINDING OF CO(2) ACTIVATES THE ENZYME.

SEQUENCE 458 AA; 50091 MM; E4AE2535 CRC32;
                                                                                                                                      RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).
PROKĀRYOTA; GRACILICUTES; ANOXYPHOTOBACTERIA; PURPLE BACTERIA;
                                                  01-OdT-1996 (REL. 34, CREATED)
01-OdT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OdT-1996 (REL. 34, LAST ANNOTATION UPDATE)
RIBULIOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN 2 (EC 4.1.1.39).
CBBM OR RBPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 58.5 KD PROTEIN IN SPOIITC-CWLA INTERGENIC REGION.
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MEDLINE: 95219086.
TAKEMARU K.-I., MIZUNO M., SATO I., TAKEUCHI M., KOBAYASHI Y.;
                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 | 3-PHOSPHO-D-GLYCERATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; | U23145; G727418; -.
PHOTOȘYNTHESIS; CARBON DIOXIDE FIXATION; PHOTORESPIRATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.6%; Score 56; DB 8; Length 458;
Larity 55.6%; Pred. No. 6.01e+00;
Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                         458 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILIUE, 96084975.
MEDIGUE C., MOSZER I., VIARI A., DANCHIN A.;
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MICROBIOLOGY 141:323-327(1995).
                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 AA; 500c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                            RHODOSPIRILLACEAE.
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 sfprqflhy 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACILLUS SUBTILIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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LT 9
RBL2 RHOCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YQBA_BACSU
P45917;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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   RESULT
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GENETICS 130:471-498(1992).

-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME COMPLEX. CO I IS THE CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A 3 AND COPPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ERALLILALICARINGE.

SUBCELIDIAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSKEMBRANE DOMAINS.

- STMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY. SA54253; G5594965; -...

EMBL, X54253; G5594965; -...

PROSITE; PS00077; COXI.

OXIDOREDUCTASE; HEME: COPPER; MITOCHONDRION; TRANSMEMBRANE;

RESPIRATORY CHAIN; INNER MEMBRANE.
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; ASCARIDIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)0 + 4 FERRICYTOCHROME C.
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                                                                                                                             Length 510;
                                                                                                           Score 56; DB 11; Length DLV, Pred. No. 6.01e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 525;
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2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRON (HEME A3) (PROBABLE)
IRON (HEME A) (PROBABLE).
A6124BE2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRON (HEME A) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                         ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COPPER B (PROBABLE)
COPPER B (PROBABLE)
COPPER B (PROBABLE)
COPPER B (PROBABLE)
                                                                                                                                                                                                                                                                                              01-MAR-1992 (REL. 21, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-FCB-1996 (REL. 33, LAST ANNOTATION UPDATE)
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
                                                                                           510 AA; 58458 MW; 433165AB CRC32;
GENE 165:GC37-GC51(1995).
-1- SIMILARIY: STRONG, TO B.SUBIILIS XKDE.
EMBL. D32216, G1217849; -.
EMBL. D44422; G1303740; -.
SUBTILIST; BG11272; YOBA.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     678 AA.
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Pred. No.
                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-BODY WALL MUSCLE, AND EGG;
MEDLINE; 92201635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58529 MW;
                                                                                                                          Query Match
Best Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.6%;
50.0%;
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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P24881;
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YIHQ_ECOLI
P32138;
                                                                                         SEQUENCE
                                                                                                                       Query Match
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PIR; A35726; A35726
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                                                                                                                    STRAIN-S288C
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SEQUENCE
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S FINA RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON RANGE SON
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GOMPELS U.A., NICHOLAS J., LAWRENCE G., JONES M., THOMSON B.J.,
MARTIN M.E., EFSTATHIOU S., CRAXTON M., MACAULAY H.A.;
VIROLOGY 209:29-51(1995).
-: FUNCTION: PROVIDES THE PRECURSORS NECESSARY FOR DNA SYNTHESIS.
-: CHALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE DIPHOSPHATE + OXIDIZED
THIOREDOXIN + H(2)0 = RIBONUCLEOSIDE DIPHOSPHATE + REDUCED
                                                                                                ESCÜERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
HYPOTHETICAL 77.2 KD PROTEIN IN GLNA-FDHE INTERGENIC REGION (F678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- PATHWAY: FIRST REACTION IN THE DNA REPLICATION PATHWAY.
-:- SUBUNIT: HEPERODIMER OF LARGE AND A SMALL CHAIN.
-:- SIMILARITY: HIGH TO OTHER BUKARYOTIC, PROKARYOTIC, AND VIRAL RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE LARGE CHAINS.
EMBL; X83413, 6854007; --
OXIDOREDUCTASE: DNA REPLICATION.
SEQUENCE 804 AA; 93352 MW; B59993FD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SECUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (EC 1.17.4.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MG1655;
MG1655;
MG1655;
MG1656;
MG1871 G. III, BURLAND V.D., DANIELS D.L., BLAITNER F.R.;
NUCLEIC ACIDS RES. 21:3391-3398(1993).
PMB1: 19201; G304982;
PMB1: 1940822.
ECOGENE; G511843; YHQ.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                          Score 56; DB 11; Length 678; Pred. No. 6.01e+00; 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.6%; Score 56; DB 8; Length 804; 50.0%; Pred. No. 6.01e+00; artive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                     678 AA; 77249 MW; 8D74E4AE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      804 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
27, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                            wery Match 49.6%; est Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     larity 50.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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(REL. 34, I
(REL. 34, I
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2 TFPPKYLHYD 11
                                                                                                                                         ENTEROBACTERIACEAE
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5 PKYLHYDEET 14
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01-OCT-1993 (REL.
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YNN2_YEAST

P53914;

01-OCT-1996 (

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P52343;
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DT 01
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HISTOLINE; 90105318.
SHEARES B.T., WHITE S.S., MOLOWA D.T., CHAN K., DING V.D.-H.,
SHEARES B.T., WHITE S.S., MOLOWA D.T., CHAN K., DING V.D.-H.,
KROON P.A., BOSTEDOR K.G., KARKAS J.D.;
BIOCHEMISTRY 28:8129-8135(1999).
-!- FUNCTION: CATALYZES THE SEQUENTIAL CONDENSATION OF ISOPENTENYL
PYROPHOSPHATE WITH THE ALLYLIC PYROPHOSPHATES, DIMETHYLALLYL
PYROPHOSPHATE, AND THEN WITH THE RESULTRANT GERANYLEYROPHOSPHATE
-!- CATALYTIC ACTIVITY: DIMETHYLALLYL DIPHOSPHATE - ISOPENTENYL
DIPHOSPHATE = PYROPHOSPHATE + GERANYL DIPHOSPHATE
-!- CATALYTIC ACTIVITY: GERANYL DIPHOSPHATE + ISOPENTENYL
DIPHOSPHATE + TRANS, TRANS-FARNESYL DIPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (REL. 13, CREATED)
01-FEB-1996 (REL. 33, LAST SROUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE)
DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLLTRANSFERASE (EC 2.5.1.1) /
GERANYLITRANSTRANSFERASE (EC 2.5.1.1) / (KIAAO032).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
HYPOTHETICAL 119.3 KD PROTEIN IN FPR1-TOM22 INTERGENIC REGION.
YNL132W OR N1216 OR N1858.
SACCHAROWICES CEREVISIAE (BAKER'S YEAST).
BUKARYOHA, FUNDI, ASCOMYCOTINA, HEMIASCOMYCETES.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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-: PATHWAY: ISOPRENE BIOSYNTHESIS.
-: SUBCELLULAR LOCATION: CYTOPLASMIC.
-: SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER FPP SYNTHETASE, GGPP SYNTHETASE AND HEXAPRENYL PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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NOMURA N., MIYAJIMA N., KAWARABAYASHI Y., TABATA S.;
SUBMITTED (MAR-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                 283 290 ATP (POTENTIAL).
1056 AA; 119347 MW; CF839C98 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 11; I
Pred. No. 6.01e+00;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 90170972.
WILKIN D.J., KUTSUNAI S.Y., EDWARDS P.A.;
J. BIOL. CHEM. 265:4607-4614(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                            EIN; ATP-BINDING.
290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 8-353 FROM N.A.
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Conservative
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                                                                                                                                                                                                  MEDLINE; 96109932.
                                                                                                                                                SEQUENCE FROM N.A.
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Query Match
Best Local Similarity 33.3%; Pred. No. 8.97e+00;
Matches 4; Conservative 7; Mismatches 1; Indels 0;
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rch completed: Tue Dec 2 14:52:14 1997 time : 10 secs.

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MPsrch_nn n.a. n	ibution rights by IntelliGenetics, Inc. database search, using Smith-Waterman algor
Run on: Tue ular output not ge	e Dec 2 14:43:20 1997; MasPar time 990.46 Seconds 1313.995 Million cell updates/sec generated.
Title: >US-08- Description: (1-1185 Perfect Score: 1185 N.A. Sequence: 1	08-915-004-8 185) from USO8915004.seq 1 ATGAACAACTTGCTGTGCTGTAAAAATAAGCTGCTTATAA 1185 1 AACTTGTTGAACAACAAGACGACGACATTTTATTCGACGAATATT
Scoring table: TABLE Gap 6	Le default
Nmatch STD : Dbase	se 0; Query 0
Searched: 362067	067 seqs, 549138275 bases x 2
Post-processing: Minimum Listing	nimum Match 0% sting first 45 summaries
Database: embl 1: 9:	=mbl-new3 1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC 17:VIR
Database: gent 18 25 23	CT1 19:BCT2 CCT8 26:BCT9 EN3 32:HTG1
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Database: genb	nbank-new3 106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV 110: MAM 113:NFT 114:PHG 115:FLN 116:PR11 117:PR12 119:EGN 110:EWN 170:HTM 121:VDT
Database: u-en	150_99 :part1
Statistics: Mean	n 11.245; Variance 4.362; scale 2.578
Pred. No. is the r score greater thar and is derived by	the number of results predicted by chance to have a than or equal to the score of the result being printed, d by analysis of the total score distribution.

SUMMARIES

S	4	Query Match		DB 57 57	1	tion e 5 fro e 5 fro	paten paten	ed. No 40e-06 05e-05
w 4 €	7 7 7 8 8 7 2 8 7			111 8 111		cha tha f		1.84e-0.84e-0.1.90e-
9 / 8	2 2 2 2 2 2		35 144 193	8 51 49		ha f ibri us s	57k aci (G	90e-0 90e-0 90e-0
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21112	22222	00000	1256 1380 1388 1388	47 91 86 118	OCSP17GN RNINL1R2A MMTNFR2A MMTNFR2A	in gar	lterleu or necr	1.34e+01 1.34e+01 1.34e+01 1.34e+01
7 7 7 7 7 7 7 7 7 7	53357		1146 1185 185 185 185	67 1117 75 65	SCYOLO85C HSLIPA4 HSLIPA4 SCDNAFUS2	revis apien piens	iae chromoso s LIPA gene, LIPA gene, iae fus2 gen	400+0 400+0 400+0 40+0
222 232 44	22 22 23 23 23 23 23 23 23 23 23 23 23 2		255 278 302 311	55 91 81 81	IO9123 RATPKATB5 YSCGLN3 HUMLD78B	Sequence 5 from Rat peroxisoma S.cerevisiae n: Human LD78 beta	n Paten 1 3-ket itrogen a gene.	34e+0 34e+0 40e+0 34e+0
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300 300 307	222		705	88 88 70	CEU30248 MUSA1CC EAAMASL	se mRN nylova	mouse	34e+0
33 33	222		2692 2868 3858	38 37	CEM03B6 CELF42H10 CELF55C12	orhab elegan orhab	elegan nid F42 elegan	.34e+0 .34e+0 .40e+0
334 35	222		3930 4026	65 77 65	SCCHXVORF HSU159B9 SC9959	erevis an DNA erevis	DNA for uence fr chromoso	.34e+0 .34e+0 .34e+0
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0 1 7	22 22 21		1857 25791 10	80 103 56	HUMFMR1S PBU42580 I14734	sapiens framecium bu	agile saria m pate	34e+01 1.34e+0 .01e+01
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Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use to
                                                               snggtdgnrsgadsygssktamtsrnrt-gktannavdsrnmgdasvgsdkntkkhakns 164
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                           2; Gaps
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Oxytricha fallax

Oxytricha fallax

Eukaryotes; Alveolata; Ciliophora;

Hypotrichs; Stichotrichida; Oxytricha.

I (bases I to 334)

Doak, T.G., Doerder, F.P., Jahn, C.L. and Herrick, G.

A proposed superfamily of transposase genes: transposon-like
Query Match 2.7%; Score 32; DB 57; Length 215; Best Local Similarity 18.8%; Pred. No. 2.40e-06; Matches 26; Conservative 54; Mismatches 56; Indels
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76; Mismatches 88; Indels
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Patent: US 5569830-A 5 29-OCT-1996;
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Sequence 5 from patent US 5569830.
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Best Local Similarity 15.2%;
Matches 30; Conservative
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(pases 1 to 354)
Witherspoon, D.J., Doak, T.G., Williams, K., Seger, J. and Herrick, G. Selection on the protein-coding genes of the TBEI family of transposable elements in the ciliates Oxytricha fallax and O.
                                                                                                                                                                                                                                                                                                                                                                         Submitted (II_FEB-1997) Oncological Science, University of Utah, School of Med. RmSC334, USA, UT 84132, USA Location/Qualifiers
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13-WAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57KD zinc finger/protein chimera gene, partial
elements in ciliated protozoa and a common 'D35E' motif
Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
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3 (Dases 1 to 354)
Doa k, Ass. Williams, K., Witherspoon, D.J. and Herrick, G. Direct Submission
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Doak T.G., Doerder F.P., Jahn C.L., Herrick G.;

"A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common '035E' motif";

Proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
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hypotrichs; Stichotrichida; Oxytrichidae; Oxytricha.
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/db_xref="piD:g1881676"
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13-MAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein chimera gene, partial
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Doak T.G., Doerder F.P., Jahn C.L., Herrick G.;

"A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common '035E' motif", Proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
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"Selection on the protein-coding genes of the TBE1 family of
transposable elements in the ciliates Oxytricha fallax and O.
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Eukaryotae; mitochondrial eukaryotes; Alveolata; Ciliophora;
hypotrichs; Stichotrichida; Oxytrichidae; Oxytricha.
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/product="57kD zinc finger/protein chimera"
/transl_table=6
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/codon_start=1
/product=157kD zinc finger/protein chimera"
/db_xref="PID:g1881676"
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Best Local Similarity 23.7%;
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PCR product that represents many transposon templates"
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PCR product that represents many transposon templates"
<1..>354
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A proposed superfamily of transposase genes: transposan-like
elements in ciliated protozoa and a common 'D35E' motif
proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
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hypotrichs; Stichotrichida; Oxytricha.
                                                     Submitted (11-FEB-1997) to the EMBL/GenBank/DDBJ databases.
Oncological Science, University of Utah, School of Med. Rm5C334,
USA, UT 84132, USA
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Doak, T.G., Williams, K., Witherspoon, D.J. and Herrick, G.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"57kD zinc finger/protein chimera" /transl_table-6
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     Doak T.G., Williams K., Witherspoon D.J., Herrick G.;
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Sequence 354 BP; 106 A; 42 C; 41 G; 54 T; 111 other;
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Best Local Similarity 30.1%; Pred. No. 1.84e-03;
Matches 25; Conservative 33; Mismatches 24,
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/strain="9D1"
                                                                                                                                                                                                                                   /organism="Oxytricha fallax"/strain="9D1"
                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                         /transposon="TBE1"
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Oxytricha fallax
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'tissue_type="retina"
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                                                                                                                                                                                                                                                                                                                                                  /note="putative"
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Best Local Similarity 77.8%;
Matches 35; Conservative
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Carassius auratus
                                                                                                                                                                                  Unpublished (1993)
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                                                                                 Carassius.
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ORGANISM
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                                                                                                                                           TITLE
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/translation="VDLDVSKPDLTPALKETRAGFEAMATSNNGETEEWYRSKFADLT
DAASRNTEALROAKOEANEYROIOGUTCDLESLRGSNNESERERFIETBAG
YQDTVARLEDBIQMAKEEMARHLOEYQOLLUNKLALDIEIAYTRKLLEGEESRITVPV
ONFTRIQFRDTSLDFKLTPEAHVKRSIVVRTVETROGEIIKESTTERNDLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Description: glial fibrillary acidic protein, GFAP;
Method: conceptual translation with partial peptide
sequencing. This sequence comes from Fig. 2"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae;
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                                                                                                                                                                                                                                                                                                                            Sb6477 1441 bp mRNA VRT 17-DEC-1993 glial fibrillary acidic protein (clone 2) [Cyprinus carpio-carp, s66477
                                                                                                                                                                       rgcdagrgaryhhyhdwargwbgydgwgcyykaayaagcwagmgarwyaswrtrygtaar 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 139069] from the original journal article. This sequence comes from Fig. 1.

Location/Qualifiers
                                                                                                                    Gaps
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Cohen,I., Shani,Y. and Schwartz,M.
Cohen,I., Shani,Y. and Schwartz,M.
Cohening and characteristics of fish glial fibrillary acidic protein: implications for optic nerve regeneration
J. Comp. Neurol. 334 (3), 431-443 (1993)
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                                                 2.1%; Score 25; DB 8; Length 354;
Local Similarity: 23.7%; Pred. No. 1.90e-01;
les 23; Conservative 38; Mismathham
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                         Sequence 354 BP; 106 A; 42 C; 41 G; 54 T; 111 other;
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Pred. No. 1.90e-01;
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        HQYAYKVYPFNYLX"
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Best Local Similarity 77.8%;
Matches 35; Conservative
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                                                                  Query Match
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FEATURES

CDS

BASE COUNT

ORIGIN

DEFINITION

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KEYWORDS SOURCE

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SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS

TITLE

JOURNAL MEDLINE

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//dLxref="PID: 90LINDRPASYIEKVRFLEQONKMLVAELNQLRGKEFSRLGDIYQ
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VDBALNRVQUERKIDALQDEISFLERVHEERNROLGBQILAQQVHYDLNYGRPDLTA
ALKEIRAQFERMATSNNQETBEWYRSKFADLTDAAGRNAEALRQAKOFBNEYRRQIQG
LTCDLESLRGSNRESRRAFSRFADLTDAAGRNAEALRQAKOFBNEYRRQIQG
LTCDLESLRGSNRESRRAFSRFADLTDAAGRNAEALRQAKOFBNAFRRQIQG
DLLNYKLALDIEIRQLKERGEBRA IETAGYQDTYARLDDEIQUHKEEBMARHLQPY
QDLLNYKLALDIEIDATYRKLLGGEBERRITGRAYQUFTNLQFRDTSLDTKLTPEAHVKRS
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Cambridgeshire, CB10 1SA, UK. E-mail enquires:

Cambridgeshire ac.uk Clone requests: clonerequest@sanger.ac.uk

IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae;
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Glasgow, E. and Schechter, N.
Nucleotide sequence of a GFAP - like intermediate filament cDNA
from Goldfish retina
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SEQUENCING IN PROGRESS *** from clone
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Bukaryotae; intochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 115419)
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 /transl_table=6
/db_xref="PID:91881682"
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                                                                                                                                            * This sequence is unfinished. When sequencing is complete, the sequence data presented in this record will be replaced *by a single finished sequence with the same accession number. Location/Qualifiers
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Oncological Science, University of Utah, School of Med. Rm5C334,
USA, UT 84132, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Witherspoon D.J., Doak T.G., Williams K., Seger J., Herrick G., "Selection on the protein-coding genes of the TBEL family of transposable elements in the ciliates Oxytricha fallax and O. trifallax";
                                                                                                                *** WARNING: Phase 1 High Throughout Genome Sequence ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3-MAR-1997 (Rel. 51, Created)
13-MAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein kinase gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 94134747.

Doak T.G., Doerder F.P., Jahn C.L., Herrick G.;

A proposed superfamily of transposase genes: transposon-like elements in ciliated procesoa and a common 'D35E' motif";

Proc. Natl: Acad. Sci. U.S.A. 91:942-946(1994).
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hypotrichs; Stichotrichida; Oxytrichidae; Oxytricha.
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Pred. No. 8.23e-01;
0; Mismatches 8;
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/strain="9D1"
/transposon="TBE1"
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                                                                                                                                                                                                                                              'chromosome="22"
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Sest Local Similarity 80.0%;
Aatches 32; Conservative
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/translation="HTRDLXKHLLKAXKKXXEXEXXXXXLKXLNKRKAREXXXXXXXX
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Oxytricha fallax.

Oxytricha fallax.

Eukaryotes; Alveolata; Ciliophora; hypotrichs; Stichotrichida; Oxytricha.

I bases 1.0 370)

Doak,T.G., Doerder,F.P., Jahn,C.L. and Herrick,G.

A proposed superfamily of transposase genes; transposon-like elements in ciliated protozoa and a common 'D35E' motif Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
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Doak,T.G., Williams,K., Witherspoon,D.J. and Herrick,G.
Direct Submission
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1.9%; Score 22; DB 111; Length 370;
Best Local Similarity 32.5%; Pred. No. 1.34e+01;
Matches 27; Conservative 28; Mismatches 27; Indels
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/transl_table=6
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                                                                                                                                                    Sequence 370 BP; 116 A; 43 C; 48 G; 69 T; 94 other;
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/strain="9D1"
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Direct Submission
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/note="3' untranslated region is identical for both 0.9 KB
AND 1.1 KB mRNAS"
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NLLEKREKTHFDPAEWGAKVDDRFYNNHAFQEHESEKCEAEEKSGSVTEEETPVLTID
SEDDKDKEEMAALKIQAAFRGHLAREDVKKIRTNKAEEFTEENN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-7AM-1993) O'Rand M. G., University of North Carolina at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel Hill, North Carolina, USA, 27599-7090

Hill, North Carolina, USA, 27599-7090

(bases I to 1256)
O'Rand,M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-APR-1994) O'Rand M. G., University of North Carolina at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel Hill, North Carolina, USA, 27599-7090
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736 CIGCIGAAGITAIGGAAACAICAAAACAAAGACCAAGAIA-IAGICAAGAAGAICAICCA 794
                                                                                                                                                                                                                                   Oryctolagus cuniculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (Dases 1 to 1256)
Richardson, R.T., Yamasaki, N. and O'Rand, M.G.
Sequence of a rabbit sperm zona pellucida binding protein and localization during the acrosome reaction
95046885
                                                                                                                                       02-MAR-1995
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/cell_type="spermatogenic"
/clone_lib="Rabset"
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                              172 accwmytrrcmtchgarrtmacw 194 | :::|::|::|:|:|:|795 AGATATTGACCTCTGTGAAAACA 817
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O.cuniculus SP17 gene.
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Best Local Similarity 69.6%;
Matches 39; Conservative
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European rabbit.
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Submitted (24-MAY-1993) Jesper Bristulf, Department of Neurochemistry and Neurotoxocology, Arrheniuslaboratories of Natural Sciences, Stockholm University, Stockholm, S-106 91, Sweden Location/Qualifiers
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RORDFKSELELBGGEPVVLTCPLPVHPSDTSSSSSLESSSGVLFDGEPRWWVD
DTLWYLPAVQQDSGTYTCTFRNASHCBQMSLELKVFRVTBASFPLVSYLOISALSSTC
LLVCPDLKEFISSRTDGKIQWYKGSILLDKGNKKFLSAGDPTRLLISNTSMGDAGYTR
GTRETHSFELSWRGITTERPHVYITSPLPTISPLTSPALGSRTLYPGKYFLGT
GTSSNTIVWWANANSFISVAFTSVAFFELHQYSRNDENYPSVSLIFDPWTKEDLNT
DFKCVATNPFYERDLYPGKYFLDGT
GTSSNTIVWWANANSFISTSVAFFRGYLHQYSRNDENYPGSLIFDPWTKEDLNT
DFKCVATNPFYERDLYPTVKFUSAFFRGYTHQYSRNDENYPGSNIFFDANT
DFKCVATNPFYERDLYPTVKFUSAFFRGYTHQYSRNDENYPGSLIFFDANT
DFKCVATNPFYERDLYPTVKFUSAFFRGYTHQYSRNDENYPGSLIFFDANT
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DFKCVATNPFREFYERDLYPTVKFUSAFFRGYTHQYSRNDENYPGSLIFFDANT
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DFKCVATNPFTFREFYERDLYPTVKFUSAFFRGYTHQYSRNDENYPGSLIFFDANT
DFKCVATNPFTFREFYERDLYPTVKFUSAFFRGYTHQYSRNDENYPGSTFFRGYTHQYSRNDENYPGTANTFRCKRQAGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murinae; Rattus.
1 (bases 1 to 1380)
Bristulf,J., Gatti,S., Malinowsky,D., Bjork,L., Sundgren,A.K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-1 stimulates the expression of type I and type II interleukin-1 receptors in the rat insulinoma cell line Rinm5F; sequencing a rat type II interleukin-1 receptor cDNA Bur. Cytokine Netw. 5 (3), 319-330 (1994)
                                                                                                                                                                                             16-DEC-1994
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/db_xref="PID:9311408"
/db_xref="SWISS-PROT:P43303"
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M.musculus tumor necrosis factor receptor 2 mRNA.
X76401
                                                                                                                                                                                     R.norvegicus interleukin-1 receptor type 2. 222812
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Pred. No. 1.34e+01;
0; Mismatches 2;
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/cell_line="RINM5F"
124..1374
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                                                                                                                                                                                 1380 bp
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Bristulf, J.
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Powell, E.E.
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Best Local Similarity 92.3%;
Matches 24; Conservative
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/gene="murine tumour necrosis factor receptor
/note="silent"
/replace="c"
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921
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Direct Submission
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PGQYVKHFCKRTSDTVCADCEASMYTOVWNOFRTGLESCSSCSTDQVETRACTKOQNR
VCACEAGRYCALKTHSGSCROCMILSKCGPGFGVASRAPNGNVLCKACAPGTFSDTT
SSTDVCRPHRTCSILLAIPGNASTDAVCAPESPTLSAIPRILVSQPEPTRSOPLOGEP
GPSQTPSILTSLGSTPIIEQSTKGGISLPIGLIVGYTSLGLLMLGLVNCFILVQRKKK
QARVMARAQGSQEARASRALSGSSHGSHGHTWNYCIVVCSSDBISSQCSSGASATV
GDPDAKPSASPKDEQVPFSQEECPSQSPYETTETLQSHEKPLPLGVPDMGMKPSQAGW
                                                                                                                                                      Powell,E.E., Wicker,L.S., Peterson,L.B. and Todd,J.A. Allelic variation of the type 2 tumor necrosis factor receptor gene Mann. Genome 5 (11), 726-727 (1994)
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Submitted (26-NOV-1993) E.E. Powell, c/o John Todd, Level 6
Nuffield Dept of Surgery, The John Radcliffe Hospital, Oxford,
2 (bases 1 to 1388)
Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A.
Amino acid variation in the tumor Necrosis factor receptor 2 is linked to autoimmune diabetes in NOD mice
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replace(1317, "g")
/gene="murine tumour necrosis factor receptor 2"
/note="silent"
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/note="silent"
replace(1262, g")
/gene="murine tumour necrosis factor receptor 2"
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/note="Thr to Ile"
replace(489,"t")
/gene="murine tumour necrosis factor receptor 2"
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/note="Phe to Ile"
replace(921,"c")
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/note="silent"
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/gene="murine tumour necrosis factor receptor /note="silent"
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/gene="murine tumour necrosis factor receptor
/note="ser to phe"
/place(1047, "t")
/gene="murine tumour necrosis factor receptor
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/note="Ser to Thr"
replace(278, "t")
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Pred. No. 1.34e+01;
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                                                                                                                                                                                                                                                                                      /strain="NOD"
/chromosome="4 (distal region)"
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                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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Best Local Similarity 64.1%;
Matches 50; Conservative
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ORIGIN
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SSIDVCRPHRICSILAIPGNASTDAVCAPESPILSAIPRILYVSQPEPIRSQPLDQEP
GPSQTPSILISLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCFILVQRKKK
PSCLQRDAKVPHVPDEKSQDAVGLEQQHLLITAPSSSSSSLESSASAGDRRAPPGGHP
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Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A.

Allelic variation of the type 2 tumor necrosis factor receptor gene

Mamm. Genome 5 (11), 726-727 (1994)
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PGQYVKHFCNKTSDTVCADCEASMYTQVWNQPRTCLSCSSSCSTDQVETRACTKQQNR
VCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTT
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GDPDAKPSASPKDEQVPFSQEECPSQSPYETTETLQSHEKPLPLGVPDMGMKPSQAGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (26-NOV-1993) E.E. Powell, c/o John Todd, Level 6
Nuffield Dept of Surgery, The John Radcliffe Hospital, Oxford, UK
2 (bases 1 to 1388)
Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A.
Amino acid variation in the tumor Necrosis factor receptor 2 is
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae;
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                                                               111 TCAGCTGTTGTGTACAAATGTCCTCCTGGTACCTAAAAAACAACACTGTACAGAAA 170
                                                                                                                                                                                                                                                                                                                                   17-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="murine tumour necrosis factor receptor 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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/replace="c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //gene="murine tumour necrosis factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="murine tumour necrosis factor receptor/note="Phe to Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="murine tumour necrosis factor receptor
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                                                                                                                                                                                                                                                                                                                            MMINFR2A 1388 bp RNA ROD
M.musculus tumor necrosis factor receptor 2 mRNA.
X76401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="4 (distal region)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour necrosis factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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Best Local Similarity 64.1%; Pred. No. 1.34e+01;
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variation
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Search completed: Tue Dec 2 15:19:52 1997
Job time : 2192 secs.

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(ME)
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l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
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                                                                                                                                                                                             MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
                                                                                             Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
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Perfect Score:
N.A. Sequence:
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					SUMMARIES			
1		ي م						
NO.	Score	Match	Match Length DB	DB	Ü	Description		Pred. No.
п	1059	89.4	1206	28	T36685	Osteoclastogenesis in	sis in	0.00e+00
7	1057	89.2	1206	78	T33161	Mutated OCIF, O	OCIF-C1	0.00e+00
m	1055	89.0	1206	27	T33165	Mutated OCIF, 0	OCIF-C2	0.00e+00
4	1055	99.0	1206	27	T33164	Mutated OCIF, O	OCIF-C2	0.00e+00
Ŋ	1055	0.68	1206	58	T33162	Mutated OCIF, O	OCIF-C2	0.00e+00
9	1053	88.9	1206	27	T33163	Mutated OCIF, O	OCIF-C2	0.00e+00
7	1051	88.7	1200	27	T33172	Mutated OCIF, O	OCIF-CL	0.00e+00
۵	1028	86.8	1182	27	T33178	Mutated OCIF, O	OCIF-CB	0.00e+00
σ	1017	85.8	1173	58	T35475	Human tumour ne	necrosis	0.00e+00
10	923	77.9	1083	27	T33166	Mutated OCIF, O	OCIF-DC	0.00e+00
11	907	76.5	1056	27	T33173	Mutated OCIF, O	OCIF-CC	0.00e+00
12	890	75.1	1080	27	T33167	Mutated OCIF, O	OCIF-DC	0.00e+00
13	806	68.0	996	27	T33179	Mutated OCIF, O	OCIF-CS	0.00e+00
14	765	64.6	1080	27	T33168	Mutated OCIF, O	OCIF-DC	0.00e+00
15	671	56.6	984	27	T33171	Mutated OCIF, O	OCIF-DD	0.00e+00

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 9.128; Variance 5.035; scale 1.813

Statistics:

89.4%; Score 1059; DB 28; Length 1206;

Query Match

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16 669 56.5 819 17 649 54.8 1080 18 453 38.2 981 18 453 38.2 981 19 444 37.5 594 20 413 34.9 564 21 331 33.0 10190 22 22.5 22.6 458 22 26.2 2.6 22.6 458 22 26.2 2.6 22.6 458 22 26.2 2.6 22.6 458 22 26.2 2.6 22.6 458 24 265 22.4 458 25 26.2 2.6 22.8 255 27 114 28 33 3.3 204 31 33 3.3 204 31 33 3.3 204 32 2.7 114 41 32 2.7 114 41 32 2.7 114 41 32 2.7 114 42 33 2.8 114 31 33 3.3 2.8 114 32 2.7 114 43 30 2.5 114 44 30 2.5 114 45 30 2.5 114 45 30 2.5 114 47 32 2.7 114 48 30 2.5 114 49 30 2.5 114 41 32 2.7 114 41 32 2.7 114 42 32 2.7 114 43 30 2.5 114 44 30 2.5 114 45 30 2.5 114 45 30 2.5 114 47 32 2.7 114 48 30 2.5 114 49 30 2.5 114 49 30 2.5 114 49 30 2.5 114 41 32 2.7 114 41 32 2.7 114 42 30 2.5 114 43 30 2.5 114 44 30 2.5 114 45 30 2.5 114 45 30 2.5 114 45 30 2.5 114 46 30 0.007 47 743 6 4 1230/40 48 196 4 12320/40 48 196 4 12320/40 48 196 6 6 6 8 8 104 48 196 6 6 6 8 8 104 48 196 6 6 6 8 8 104 48 196 6 6 6 8 8 104 48 196 6 6 6 8 8 104 48 196 6 6 8 8 104 48 196 6 6 8 8 104 48 196 6 6 8 8 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Location/ 163	00374054977207508. DAND MILK P ING K, Kob Ind N, Tsu 47. 25. Steoclastog tion contr 56-67; H3p sncodes the inve ff the inve ff D under r its activi day and control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of control of
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		\$ ID.				

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T 2
T33161 standard; DNA; 1206 BP.
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Similarity 98.3%;
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 7. Page 122, 183pp, Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C19S in which the 19th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption, e.g.
                                                                    1081 gtcactcagagtctaaagaagaccatcaggttccttcacaggttcacaaatgtacaaattg 1140
1000 ACCTIGAAGGGCCTAATGCACGCACTAAAGCACTCAAAGACGTACCACTTTCCCAAAACT 1059
                                                                                                              1060 GICACTCAGAGTCTAAAGAAGACCATCAGGTTCCTTCACAGCTTCACAATGTACAAATTG 1119
                                                                                                                                                                                                                     1141 tatcagaagttatttttagaaatgataggtaaccaggtccaatcagtaaaaataagctgc 1200
                                                                                                                                                                                                                                                              T33161;
22-ARF-1997 (first entry)
Mutated OCIF, OCIF-C195, coding sequence.
OSteoclattogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
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Yasuda H;
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llarity 98.2%; Pred. No. 0.000+00;
Conservative 0; Mismatches 1; Indels 21;
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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                       ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacg 300
                                                                                             280 CACAACCGCGTGTGCGAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAA 339
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                                                                       cacaaccgcgtgtgcgaatgcaaggaaggcgctaccttgagatagagttctgcttgaaa
                                                                                                                                                                                400 GITIGCAAAAGAIGTCCAGAIGGGTICTICICAAAIGAGACGICAICTAAAAGACCCCCGG
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                                                      Mutated OCIF, OCIF-C235, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 21; Gaps
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89.0%; Score 1055; DB 27; Length 1206;
Best Local Similarity 98.1%; Pred. No. 0.00e+00;
Matches 1183; Conservative 0; Mismatches 2; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 T;
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29-AUG-1996.

20-AUG-1996.

20-FBB-1995; JP-054977.

PR 21-JUL-1995; JP-207508.

PA (SNOW) SNOW BRAND MILK PROD CO LTD.

T GOLD M, H19438hio K, Kobayashi F, Mochizuki S, Mor Gold M, Shima N, Tsuda E, Ueda M, Yano K, Ya'

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                                                                                                                                                          osteoporosis; ss.
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LT 3 T33165 standard; DNA; 1206 BP.

RESULT

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                                                                                                                                                                                                                                                                                                                                                               AACAAAGACCAAGATATAGTCAAGAAGATCATCCAAGATATTGACCTCTGTGAAAACAGC 819
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Mutated OCIF, OCIF-C22S, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                    460 AGAAAACACACAAATTGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACA
                                                                                                                                              ctgtgtgtgaggaggcattcttcaggtttgctgttcctacaaagtttacgcctaactggctt
  |agaaaacacacaaattgcagtgtctttggtctcctgctaactcagaaaggaaatgcaaca
                                                                                                                 cacgacaacatatgttccggaaacagtgaatcaactcaaaaatgtggaatagttacc
                                                                                                                                                                                                                                                                           CTGTGTGAGGAGGCATTCTTCAGGTTTGCTGTTCCTACAAAGTTTACGCCTAACTGGCTT
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20-FEB-1996, J00374.
20-FEB-1995, JP-054977.
21-JUL-1995, JP-207508.
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                                                                                            DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 36; Page 135-136; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-025s in which the 22nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 tgtgacaaatgtcctcctggtacctacctaaaacaaccactgtacagcaaagtggaagacc 180
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Best Local Similarity 98.1%; Pred. No. 0.00e+00;
Matches 1183; Conservative 0; Mismatches 2; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                   264 T;
                                               Yasuda H;
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(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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                                                                                P-PSDB; R99934.
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This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C20S in which the 20th Cys residue in the mature ocif protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto eation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                aacaaagaccaagatatagtcaagaagatcatccaagatattgacctctgtgaaaacagc 840
                       700 AAACGGCAACACACACAACAACAACAACTTTCCAGCTGCTGAAGTTATGGAAACATCAA 759
                                                              841 gigcagcggcacaitggacaigciaaccicaccitcgagcagcitcgiagcitgaiggaa
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Ueda M, Yano K,
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20-FEB-1995; JP-05497.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GCCO M, Higashio K, Kobayashi F, MocNakagawa N, Shima N, Tsuda E, Ueda M, WPI; 96-402320740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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T33162 standard; DNA; 1206 BP.
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TTATAA 1185
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in the treatment and prevention of disorders of bone resorption,
                                                                                                                           2; Indels 21;
                                                                               Score 1055; DB 28; Length 1206;
Pred. No. 0.00e+00;
0; Mismatches 2; Indels 21;
                                            264 T;
                                            270 G;
                                            283 C;
                                              389 A;
                                                                                    89.08;
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Conservative
                                              1206 BP;
                                                                                                          Best Local Similarity
Matches 1183; Conser
                          osteoporosis
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Goto M. Higashin K. Kobayash F. Mochizuki S. Morinaga T;
Nakagawa N. Shima N. Tsuda E. Ueda M. Yano K. Yasuda H;
Nakagawa N. Shima N. Tsuda E. Ueda M. Yano K. Yasuda H;
NPI: 96-402120/40.

P-PSDB: R99933.

DNA ehcoding osteoclastogenesis inhibitory factor protein - useful
for bone resorption control, esp. treatment of osteoporosis
Claim 33: Page 134-135; 183pp; Japanese.

This sequence encodes a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence encodes OCIF-C1S in which the 21st Cys residue in the mature
CC for protein is substituted by Ser. The OCIF of the invention has a
molecular weight by SDS-PAGE of 60 kD under reducing conditions and
120 kB under non-reducing conditions. The protein is adsorbed onto
cation-exchangers or heparin and its activity is lowered after 10 mins
cat 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 50 deg.C. Ocif is useful in the control of bone resorption and therefore
                                                                                                                          gtcactcagagtctaaagaagaccatcaggttccttcacagcttcacaatgtacaaattg 1140
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                                                      accttgaagggcctaatgcacgcactaaagcactcaaagacgtaccactttcccaaaact 1080
                                                                                   1000 ACCTTGAAGGGCCTAATGCACGCACTAAAGCACTCAAAGACGTACCACTTTCCCAAAACT 1059
                                                                                                                                                                 GTCACTCAGAGTCTAAAGAAGACCATCAGGTTCCTTCACAGCTTCACAATGTACAAATTG 1119
                                                                                                                                                                                                                       22-APR-1997 (first entry)
Mutated OCIF, OCIF-C21S, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                 CCCAGTGACCAGATCCTGAAGCTGCTCAGTTTGTGGCGAATAAAAAATGGCGACCAAGAC 999
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Score 1053; DB 27; Length 1206; Pred. No. 0.00e+00;
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20-FEB-1995; JF-054977.
21-JUL-1995; JF-207508.
(SNOW|) SNOW BRAND MILK PROD CO LTD.
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Local Similarity 98.0%;
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1000 ACCTTGAAGGGCCTAATGCACGCACTAAAGCACTCAAAGACGTACCACTTTCCCAAAACT
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 60; Page 143-144; 183pp. Japanese.

Claim 60; Page 143-144; 183pp. Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CL in which amino acids 379-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                      22-APR-1997 (first entry)
Mutated OCIF, OCIF-CL, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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20 FEB-1995; JP-054977,
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                    Location/Qualifiers
T33172 standard; DNA; 1200 BP
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gtcactcagagtctaaagaagaccatcaggttccttcacagcttcacaatgtacaaattg 1140
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               gtttgcaaaagatgtccagatgggttcttctcaaatgagacgtcatctaaagcaccctgt 480
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                                                                                                                   541 cacgacaacatatgttccggaaacagtgaatcaactcaaaaatgtggaatagatgttacc
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                                                             agaaaacacacaaattgcagtgtctttggtctcctgctaactcagaaaggaaatgcaaca
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Mutated OCIF, OCIF-CBst, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                           Location/Qualifiers
1..63
JT 8
T33178 standard; DNA; 1182 BP.
                            (first entry)
                                                                                                         64..1179
                                                                                                                                              29-AUG-1996, J00374.
20-FEB-1996, J00374.
20-FEB-1995, JP-054977.
21-JUL-1995, JP-207508.
                                                                                                                            'product- OCIF-CBst
                                                          osteoporosis; ss.
                                                                                                                                      WO9626217-A1.
                           22-APR-1997
                                                                                      sig_peptide
                                                                                                         mat_peptide
                                                                   Synthetic.
                                                                                                 ø
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The Priblic Kayaye.

The Annocoling osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis olden in the following sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CBst in which Gla371 is substituted with Leu and amino acids 373-380 of the mature protein have been deeleted. These anion of changes have been caused by the introduction of a restriction of the older reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 50 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tttgcaaaagatgtccagatgggttcttctcaaatgagacgtcatctaaagcaccctgt 480
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                                Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1182;
                           F, Mochizuki S,
Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1028; DB 27;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
(SNOW) ) SNOW BRAND MILK PROD CO LTD.
GOLD M, Higashio K, Kobayashi F, 1
Nakagawa N, Shima N, Tsuda E, Ueda
WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 86.8%; al Similarity 98.0%; 1156; Conservative
                                                                                                       P-PSDB; R99948
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Best Local
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New human tumour necrosis factor receptor - used to develop prods.

To treating e.g. tumours, infection, auto:immune disease, graft rejection, cytotoxicity or inflammation

Claim 1; Fig 1; 59pp: English.

The receptor binds to TNF, and in particular, TNF-beta.

The receptor and for ligands for antegonists and agonists of the receptor and for ligands for the receptor. Such agonists of the receptor and for ligands for the receptor. Such agonists and differentiation, to mediate the immune response and anti-viral response, to requiate growth and provide resistance to certain infections. The antagonists may be used therapeutically, to treat autoimmune diseases, inflammation, septic shock, to inhibit graft.

Contact of the receptor and for prevent apoptosis.

Sequence 1173 BP; 374 A; 277 C; 265 G; 257 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cocagigaccagaiccigaagcigcicagiiigiggcgaataaaaaaiggcgaccaagac 1020
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721 aaacggcaacacagctcacaagaacagactttccagctgctgaagttatggaaacatcaa 780
                                              781 aacaaagaccaagatatagtcaagaagatcatccaagatattgacctctgtgaaaacagc 840
                                                                                                                                                                                                                                                                                                       gtgcagcggcacattggacatgctaacctcaccttcgagcagcttcgtagcttgatggaa 900
                                                                                                                                                                                                                                                                                                                                                                          820 GTGCAGCGCACATTGGACATGCTAACCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAA 879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      940 CCCAGTGACCAGATCCTGAAGCTGCTCAGTTTGTGGCGAATAAAAATGGCGACCAAGAC 999
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Tumour necrosis facor; INF; receptor; INF-beta; ligand; tumour;
differentiation; immune response; autoimmune disease; inflammation;
                                                                                                                                                                                          1021 accttgaagggcctaatgcacgcactaaagcactcaaagacgtaccactttcccaaaact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tatcagaagttatttttagaaatgataggtaacctagtc 1179
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15-MAR-1995; WO-U03216.
29-MAR-1995; AC-002587.
(HUMA-) HUMAN GENOME SCI INC.
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P-PSDB; R99357.
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Length 1173;

DB 28;

85.8%; Score 1017;

Query Match

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for bone resorption control, esp. treatment of osteoporosis
Claim 42, Page 137-138; 183pp; Japanese.
This sequence encodes a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence encodes OCIF-DCR1 in which amino acids 2-42 of the mature
protein have been deleted. The OCIF of the invention has a molecular
whight by SDS-RAGE of 60 kD under reducing conditions and 120 kD under
non-reducing conditions. The protein is adsorbed onto cation-exchangers
or heparin and its activity is lowered after 10 mins at 70 deg.C or 30
in the control of bone resorption and therefore in the treatment and
prevention of disorders of bone resorption, e.g. osteoporosis.
Sequence 1083 BP; 352 A; 250 C; 246 G; 235 T;
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
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Ueda M, Yano
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20-FEB-1995; JP-05497.
21-JUL-1995; JP-207508.
(SNOW ).SNOW BRAND MILK PROD CO LTD.
GOLO M. HIGABILO K, KODBYAShI F, MOC
NAKAGAWA N, Shima N, Tsuda E, Ueda M,
WPI; 96-402320,40.
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22-APR-1997 (f
Mutated OCIF, C
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Mutated OCIF, OCIF-CC, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
            623 TTACGCCTAACTGGCTTAGTGTCTTGGTAGACAATTTGCCTGGCACCAAAGTAAACGCAG
                                                                                                        agagtgtagagagataaaacggcaacacagctcacaagaacagacttccagctgctga
                                                                                                                                                                        DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim|63; Page 144-145; 183pp; Japanese.
                                                   ttacgcctaactggcttagtgtcttggtagacaatttgcctggcaccaaagtaaacgcag
                                                                                                                                                          |agttatggaaacatcaaaaacaaagaccaagatatagtcaagaagatcatccaagatattg
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Yasuda H;
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M, Yano K,
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Moch.
Nakagawa N, Shima N, Tsuda E, Ueda M,
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This sequence encodes a mutated version of the full length stetoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CC in which amino acids 331-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. of mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. ocIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                                                                                                                                                                                                                  Match 76.5%; Score 907; DB 27; Length 1056; Local Similarity 98.0%; Pred. No. 0.00e+00; es 1033; Conservative 0; Mismatches 0; Indels 21; Gaps
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Location/Qualifiers
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M09626217-A1
29-AuG-1996:
20-FEB-1996: J00374.
20-FEB-1995: JP-054977.
21-JUL-1995: JP-207508.
21-JWL Hgashio K, Kobayashi F, Nakagawa N, Shima N, Tsuda E, Ue
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T33179 standard; DNA; 966 BP.
T33179;
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Claim 45; Page 138-139; 183pp; Japanese.
This sequence encodes a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence encodes OCIF-DCR2 in which amino acids 43-84 of the mature
protein have been deleted. The OCIF of the invention has a molecular
weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under
non-reducing conditions. The protein is adsorbed onto cation-exchangers
or heparin and its activity is lowered after 10 mins at 70 deg.C or 30
mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful
in the control of bone resorption and therefore in the treatment and
prevention of disorders of bone resorption, e.g. osteoporosis.
Sequence 1080 BP; 357 A; 243 C; 236 G; 244 T;
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                                                                    901 agettacegggaaaggaaagtgggageagaagaeattgaaaaaaeaataaaggeatgeaaa 960
                                                                                                               940 CCCAGIGACCAGAICCIGAAGCIGCICAGIIIGIGGCGAAIAAAAAIGGCGACCAAGAC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutated OCIF, OCIF-DCR2, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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ttgcagtgtctttggtctcctgctaactcagaaaggaaatgcaacacacgacaacatatg
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Pred. No. 0.00e+00;
0; Mismatches 1; Indels 0
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Yasuda H;
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i F, Mochizuki S,
Ueda M, Yano K,
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20-FEB-1996; JO0374.
20-FEB-1995; JP-204597.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LT GOLO M, Higsshio K, Kobayashi F, Nakagawa N, Shima N, Tsuda E, Ue P-SDB; R99937.
                                                                                                                                                                                                                                                                                                                                               LT 12
T33167 standard; DNA; 1080 BP.
T33167;
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Local Similarity 99.9%;
Les 891; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                849 cctgaagctgctcagtttgtggcgaataaaaaatggcgaccaagacaccttgaagggcct 908
429 ttccggaaacagtgaatcaactcaaaaatgtggaatagatgttaccctgtgtgaggaggc 488
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                              attottcaggtttgctgttcctacaaagtttacgcctaactggcttagtgtcttggtaga
                                                                                                                                                                                                                                                          654 CANTITICCTIGGCACCAAAGTAAACGCAGAGAGTGTAGAGAGGATAAAACGGCAACACAG
                                                                                                                                                                                                                                                                                                                                                              ctcacaagaacagactttccagctgctgaagttatggaaacatcaaaacaaagaccaaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tatagtcaagaagatcatccaagatattgacctctgtgaaaacagcgtgcagcggcacat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morinaga T;
Yasuda H;
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F, Mochizuki S
Ueda M, Yano K
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          This sequence encodes a mutted version of the full length
Osteoclastogenesis inhibitory factor (OCIF) of the invention. This
Sequence encodes OCIF-CSph in which amino acids 298-380 of the mature
protein have been deleted and replaced by Ser-Leu-Asp. These amino
acid changes have been caused by the introduction of a restriction
site. The OCIF of the invention has a molecular weight by SDS-PAGE of
60 kp under reducing conditions and 120 kb under non-reducing
conditions. The protein is adsorbed onto cation-exchangers or heparin
and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56
deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the
control of bone resorption and therefore in the treatment and
prevention of disorders of bone resorption, e.g. osteoporosis.
Sequence 966 BP; 301 A; 228 C; 226 G; 211 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cacaaccgcgtqtgcgaatgcaaggaagggcgctaccttgagatagagtctgcttgaaa 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 CATAGGAGCTGCCCTCCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGGGAAATACA 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGACAAATGTCCTCCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 AGAAAACACACAAATTGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACA 519
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                                                                                                                                                                                                                                                                                                                 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                                                                                                                                                                                                                                                                                                                1 ATGAACAACTTGCTGTGCTGCGCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACC 60
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                                                                                                                                                                                                                                                                                0; Indels 21;
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Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                0; Mismatches
81; Page 149; 183pp; Japanese
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 97.8%;
Matches 932; Conservative
Claim
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for bone resorption control, esp. treatment of osteoporosis
Claim 48; Page 139-140; 183pp; Japanese.

This sequence encodes a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence encodes OCIF-DCR3 in which amino acids 85-122 of the mature
protein have been deleted. The OCIF of the invention has a molecular
weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under
non-reducing conditions. The protein is adsorbed onto cation-exchangers
or heparin and its activity is lowered after 10 mins at 70 deg. C or 30
mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. or 30
in the control of bone resorption and therefore in the treatment and
                                                                 841 gtgcagcggcacattggacatgctaacctcaccttcgagcagcttcgtagcttgatggaa 900
                                                                                                                                  820 GIGCAGCGCACATIGGACATGCTAACCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAA 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutated OCIF, OCIF-DCR3, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      555
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760 AACAAAGACCAAGATATAGTCAAGAAGATCATCCAAGATATTGACCTCTGTGAAAACAGC 819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding osteoclastogenesis inhibitory factor protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gaggcattcttcaggtttgctgttcctacaaagtttacgcctaactggcttagtgtcttg
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0
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                                                                                                                                                                                                                                               880 AGCTIACCGGGAAAGAAAGTGGGAGCAGAAGACATTGAAAAAACAAIAAAGGC 932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morinaga T
Yasuda H;
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20-FEB-1996; JO0374.
20-FEB-1995; JP-2054977.
21-UT-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
P-PSDB; R99938.
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Pred. No. 0.00e+00;
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Best Local Similarity 100.0%;
Matches 765; Conservative
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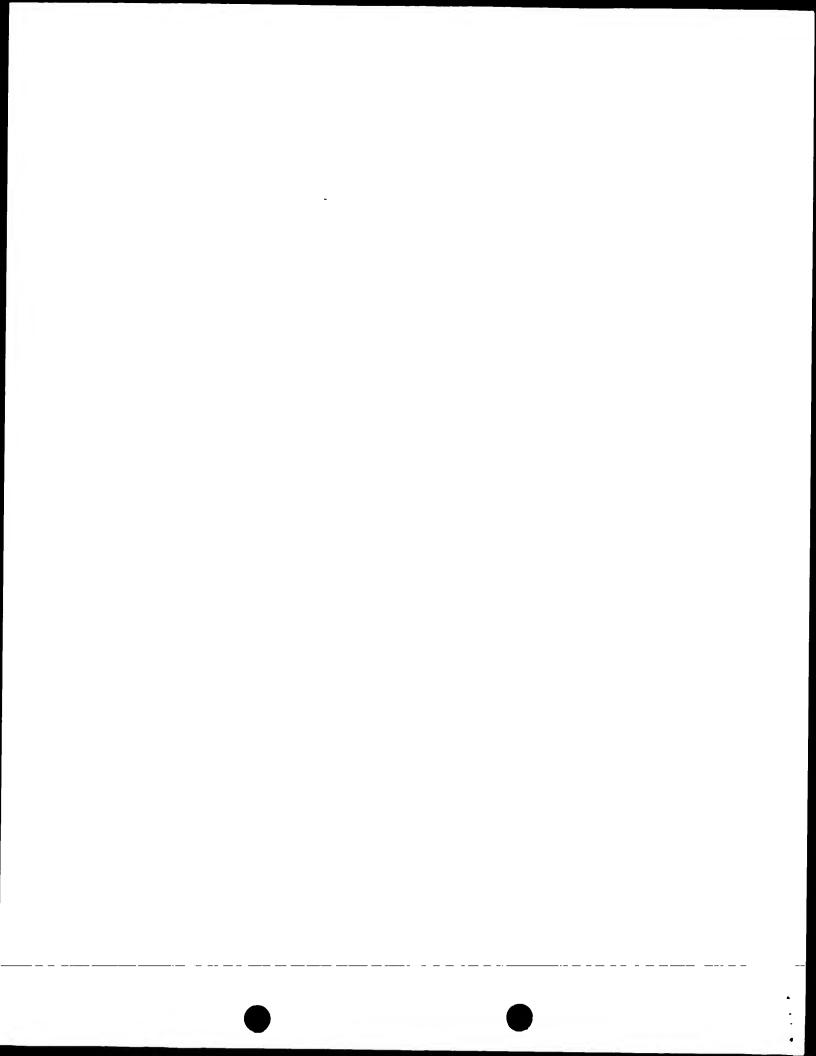
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To have been deleted. The control of the invention. This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DDD2 in which amino acids 253-326 of the mature protein have been deleted. The OCIF of the invention has a molecular protein have been deleted. The OCIF of the invention has a molecular concreducing conditions and 120 kb under concreducing conditions. The protein is addoorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                                                                                                                                                                                                                                                                            1009 GGCCTAATGCACGCACTAAAGCACTCAAAGACGTACCACTTTCCCAAAACTGTCACTCAG 1068
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Mutated OCIF, OCIF-DDD2, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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cacattggacatgctaacctcaccttcgagcagcttcgtagcttgatggaaagcttaccg
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Yasuda H;
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(SNOW ) SNOW BRAND MILK PROD CO LTD.

GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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T33171 standard; DNA; 984 BP.
T33171;
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
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 Length 984;
Score 671; DB 27; I
Pred. No. 0.00e+00;
0; Mismatches 0;
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Query Match
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc. Distribution rights by IntelliGenetics, Inc. Tue Dec 2 15:26:21 1997; MasPar time 629:50 Seconds pular output not generated.	
Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc. APSrch_nn n.a n.a. database search, using Smith-Waterman algorithm Run on: Tue Dec 2 15:26:21 1997; MasPar time 629.50 Seconds pular output not generated.	(£E)
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......TAAAAATAAGCTGCTTATAA 1185 1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 1:EST1 2:EST1 2:EST2 3:EST3 4:EST14 15:EST3 14:EST14 15:EST3 14:EST14 15:EST3 14:EST14 15:EST3 14:EST3 707517 seqs, 256659390 bases x 2 >US-08-915-004-8 (1-1185) from US08915004.seg 1185 1 ATGAACAACTIGCTGTGCTG TACTTGTTGAACGACACGAC Minimum Match 0% Listing first 45 summaries Dbase 0; Query 0 default TABLE (Gap 6 Title: Description: Perfect Score: N.A. Sequence: Comp: Post-processing: Scoring table: STD Searched: Database: Database: Nmatch

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175:EST175 176:EST176 177:EST177 178:EST178 179:EST179 180:EST180 181:EST181 182:EST182 183:EST183 184:EST184 185:EST185 186:EST181 187:EST187 188:EST188 189:EST189 190:EST190 191:EST190 191:EST190 191:EST190 196:EST198
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Statistics: Mean 11.166; Variance 1.879; scale 5.941

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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Fax: 314 286 1810
Email: est@watson.wustl.edu
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Washington University School of Medicine
Mashington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Fmail: est@wastson.wustl.edu
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INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1203 Std Error: 0.00
Seq primer: -28M13 rev2 from Anersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tacgcctaactggcttagtgtcttggtagacaatttgcctggcaccaaagtaaacgcaga 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGCCTAACTGGCTTAGTGTCTTGGTAGACAATTTGCCTGGCACCAAAGTAAACGCAGA 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gagtgtagagagataaaacggcaacacagctcacaagaacagatttccagctgctgaa 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGTGTAGAGAGGATAAAACGGCAACACACTCACAAGAACAGACTTTCCAGCTGCTGAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gttatggaaacatcaaaacaaagaccaagatatagtcaagaagatcatccaagatattga 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tctaaagcaccctgtagaaaacacacaaattcgcagtgtctttggtctcctgctaactca 61
                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 602) 1 to 602) 1 to 602) 1 to 602) 1 to 602, Clark, N., Clark, N., Clark, N., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares senescent fibroblasts NbHSF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 563; DB 195; Length 602; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              broblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="senescent fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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98.78;
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1 128 c
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est Local Similarity 98.7%;
atches 588; Conservative
                                                                                                                                                                                      Unpublished (1995)
                                                                                                                                                                                                                          Contact: Wilson RK
                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209
                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
              ORGANISM
                                                                                                                                                                      TITLE
JOURNAL
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                                                             REFERENCE
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                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 744
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SOURCE
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ostelohthyes; Sarcopterygii; Choanata; Tetrapoda; Aminota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. (pases 1 to 346)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kudaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Washerston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human clone=253126 primer=M13RPl library=Morton Fetal Cochlea vector=pBluescript SR host=SOLR cells (kanamycin resistant) Rsitel=ECORI Rsite2=XhoI The cDNA was oligo (dT) primed with an XhoI restriction enzyme recognition site and an 18 base poly dT sequence. For the 5' end, the synthesized cDNA termini were treated with T4 DNA polymerase and ECORI adaptors were ligated to the blunt ends. adaptor linker: GAATTCGGCACGAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                       862
421
                                                                                                422 tttcgtagcttgatggaaagcttaccgggaaagaaagtgggagcagaagacattgaaaa 481
                                                                                                                                                                 921
                                                                                                                                                                                                                482 acaataaaggcatgcaaacccagtgaccagatnotgaagctgctcagtttgtgggcgaata 541
                                                                                                                                                                                                                                             22-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                            863 IT-CGTAGCTTGATGGAAAGCTTACCGGGAAAGAAAGTGGGGAGCAGAAGAAAAA
                                                                                                                                                                                                                                                                                                                            542 aaaaatggcgaccaaganaccttgaaagggnctaatgcacgcacttaagcactcaa 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            н88769 346 bp mRNA EST
YW23912.r1 Homo sapiens cDNA clone 253126 5'.
H88769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMAGE Consortium (info@image.linl.gov) for
Location/Qualifiers
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RESULT

DEFINITION

ACCESSION

NID KEYWORDS

SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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AA100384 300 bp mRNA EST 28-OCT-1996 zn46h08.rl Stratagene HeLa cell s3 937216 Homo sapiens CDNA clone 550527 5'. AA100384 g1646757
                                                            Washing Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseesf@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ETPrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 300)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Wasterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 148; Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (amplcillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  865 GAAGCTGCTCGAAGGTGAGGTTAGCATGTCCAATGTGCCGCTGC 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22; DB 148;
Pred. No. 2.66e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.9%;
Best Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Conservative
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
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JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                         FEATURES
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1 (bases I to 504)

1 (hases I to 504)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevsskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 267)

Marta,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W10583 267 bp mRNA EST 05-SEP-1996 m38fl0.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 313003 5' W10583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High qality sequence stops: 299 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                    T72414 EST 01-MAR-1995 yc72a07.rl Homo sapiens cDNA clone 86196 5' similar to gb:X54486_rnal PLASMA PROTEASE C1 INHIBITOR PRECURSOR (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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0
                                                                                                                                                                                                   human clone=86196 library=Stratagene liver (#937224)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 504;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
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121 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 73.9%;
Matches 34; Conservative
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BASE COUNT

ORIGIN

FEATURES

DEFINITION

RESULT

ACCESSION

KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE

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Gaps

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LOCUS C14856 360 bp mRNA EDFINITION Human fetal brain cDNA 5'-end GEN-093D09.
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WashU-Merck EST Project
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Local Similarity 77.8%;
nes 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                        /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3
epitheliold carcinoma cells grown to semi-confluency
without induction. Average insert size: 1.5 kb; Uni-zAP XR
Vector. -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
/clone="550527"
/sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Charophyta/Embryophyta group; Embryophyta; Magnollophyta;
Lillopsida; Poales; Poaceae; Oryza.
1 (bases 1 to 330)
Sasaki, T. and Minobe, Y.
Rice cDNA from callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gagtgccttggtactttaattaagaccttcaaagcttctttttttgccattcttt 237
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Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                             215 gtaacttcattgcaaccacgaaacctgtaatacgctgtacagtaacaagtgt 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 GTACCTICATIATGACGAAGAAACCICTCATCAGCIGITGIGGACAAAIGI 132
                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 183; Length 300;
Pred. No. 2.66e-04;
0; Mismatches 15; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
1.9%; Score 22; DB 13; Length 330;
Best Local Similarity 70.4%; Pred. No. 2.66e-04;
Matches 38; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                              2 others
                                                                                                                                                                                                                                                   /dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
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National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-APR-1993) to DDBJ by:
                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
/strain="Nipponbare"
High quality sequence stop: 258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="callus"
47 c 83 g
                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                              51 g
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                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 1.9%;
Best Local Similarity 71.2%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                            43 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japan 305
Phone:0298-38-7441
Fax: 0298-38-7468
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ym62a05.rl Homo sapiens cDNA clone 163472 5' similar to SP:S32367 832367 ALPA-SNAP PROTEIN - ;.
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Deuterostomia; Chordata: Vertebrata; Gnathostomata; Osteichthyes;
Barcopterygil; Choanata; Terrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 344)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Rucaba, T., Elliston, K., Hawkins, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Marra, M., Hiller, M., Rohlfing, T., Soares, M., Tan, F., Marraton, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dmail: est@watson.wustl.edu
High quality sequence stops: 313
Source: IMAGE Consortium, LLNL, LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-SEP-1996
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1034 GAGIGCITIAGIGCGIGCATIAGGCCCTICAAGGIGICTIGGICCCCATITITI 981
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 1.22e-05
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 GCGCCCCTTGCCTGACCACTACTACACAGACAGCT 220
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house mouse.
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         source
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                                                                                                                                                                                     Direct Submission
Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otauka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd; 463-10 Ragasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
2 (sites)
Fujiwara_T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Syushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T., Meckawa,H., Nakamura,Y. and Takahashi,E.
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Source: David Sibley, Washington University
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone=tgzy27b03.rl primer=T3 library=TgRHcDNA strain=RH vector=Lambda ZAP host=XLI-Blue MRF' Rsitel=EGGRI Rsite2=XhoI foreskin fibroblast in vitro cultures. Directional cDNA was synthesized by oligo d(T) priming and cloned into EGGRI and XhoI sites of the Lambda ZAP vector using the ZAP-CDNA Synthesis Kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-APR-1996
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1 (bases 1 to 371)

Ajioka,J.a., Aslett,M.A., Dietrich,N., Dubuque,T., Kucaba,T.,
Marra,M., Sibley,L.D., Wan,K.L. and Waterston,R.A.
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toxoplasma gondii
Eukaryotae; mitochondrial eukaryotes; eukaryote crown group;
Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystida;
                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 360)
Fujiwara,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 gacttggagagttggchgaatgcaatghagtgsgcaahacamttkgaaaaaatgt 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 GATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACAGTTTGCAAAAGATGT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                            EST(expressed sequence tag); Human fetal brain.
Homo sapiens fetus brain cDNA to mRNA, clone:093D09.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 22; DB 164; Length 360;
Pred. No. 2.66e-04;
5; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/clone="093D09"
/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="brain"
83 c 75 g
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Best Local Similarity 60.7%;
Matches 34; Conservative
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                                                                 SOURCE
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(bases 1 to 385)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                              AMUB/288 385 bp mRNA EST 23-OCT-1996 mol1d06.rl Life Tech mouse embryo 10 5dpc 10665016 Mus musculus CDNA clone 553259 5' similar to gb:d03037 CARBONIC ANHYDRASE II AA087288 g1630514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
/note="Vector: pcMV-SPORT2; Site_1: Sal1; Site_2: Not1;
Cloned unidirectionally. Primer: Oligo dT. 10.5dpc
embryos. pcMV-SPORT2 vector."
/clone="553259"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murlnae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                266 gtttcgttggtgataaacatggtggagaagtccaccaacatgagctggtacaagggcaag 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Life Tech mouse embryo 10 5dpc 10665016" /dev_stage="10.5dpc embryos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                  68 GITTCCIGGGIGGTCCACTTAATGGAGATGTCCAGAAACACGAGCGCGCAGCACCAGCAAG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 2.66e-04;
0; Mismatches 3; Indels
                                                                                                                                                                                  Length 371;
                                                                                                                                                                               Score 22; DB 99; Length 371
Pred. No. 2.66e-04;
0; Mismatches 19; Indels
     gondii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trace considered overall poor quality Seq primer: -28M13 revl from Amersham High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouseest@watson.wustl.edu
/organism="Toxoplasma
/clone="tgzy27b03.rl"
/strain="RH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 ttgtagcagaagttattcttagatatga 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                               Ouery Match 1.9%;
Best Local Similarity 68.3%;
Matches 41; Conservative
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Best Local Similarity 89.3%;
Matches 25; Conservative
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DEFINITION

ACCESSION

KEYWORDS

REFERENCE AUTHORS

JOURNAL

ERENCE

AUTHORS JOURNAL

TITLE COMMENT BASE COUNT

ORIGIN

FEATURES

Matches

ORGANISM

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/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I: - oligo(dT) primer [5] to primed with a Not I: - oligo(dT) primer [5] to equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bucharjae, Metazoa, Chordata, Vertebrata, Gnathostomata, Mammalia, Butharia; Primates; Catarrhini, Hominidae; Homo.

1 (bases 1 to 410)

1 Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hutman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-1995
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WashU Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 26 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares mouse embryo NbME13.5 14.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  880 AGCTTACCGGGAAAGAAGTGGGAGCAGAAGACATTGAAAAAACAATAAA 929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yc60d04.rl Homo saplens cDNA clone 85063 5'.
T74804
g691479
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Pred. No. 2.66e-04;
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                                                                                                                                                           /organism-"Mus musculus"
                                               Seq primer: ETPrimer
High quality sequence stop: 349.
Location/Qualifiers
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High qality sequence stops: 212
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="embryo"
/dev_stage="13.5-14.5dab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 g
                                                                                                                                                                              /strain="C57BL/6J
                             Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="401252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.9%;
Best Local Similarity 72.0%;
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                                                                                                                                 1..406
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (20-FEB-1993) Genzentrum Muenchen, Laboratorium fuer
molekulare Biologie, Am Klopferspitz 18a, 8033 Martinsried,
Germany. E-mail: obermaier@vms.biochem.mpg.de
2 (bases 1 to 387)
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                                                                                                       03-FEB-1994
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
                                                                                                                         H. sapiens partial CDNA sequence; clone H23G03; single read 221693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Stratagene cDNA library Human heart, cat#936208"
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Local Similarity 86.7%; Pred. No. 2.66e-04;
hes 26. Conservative 0; Mismatches 4; Indels C
                                                                                                                                                                                                        partial cDNA sequence; transcribed sequence fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cloning vector is pBluescript SK(+); Genexpress library reference is A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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Qy 1117 TIGTATCAGAAGTTATTTTAGAAATGA 1144
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                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                     human.
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DEFINITION

RESULT

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ORGANISM

KEYWORDS

SOURCE

REFERENCE

AUTHORS

TITLE JOURNAL

COMMENT

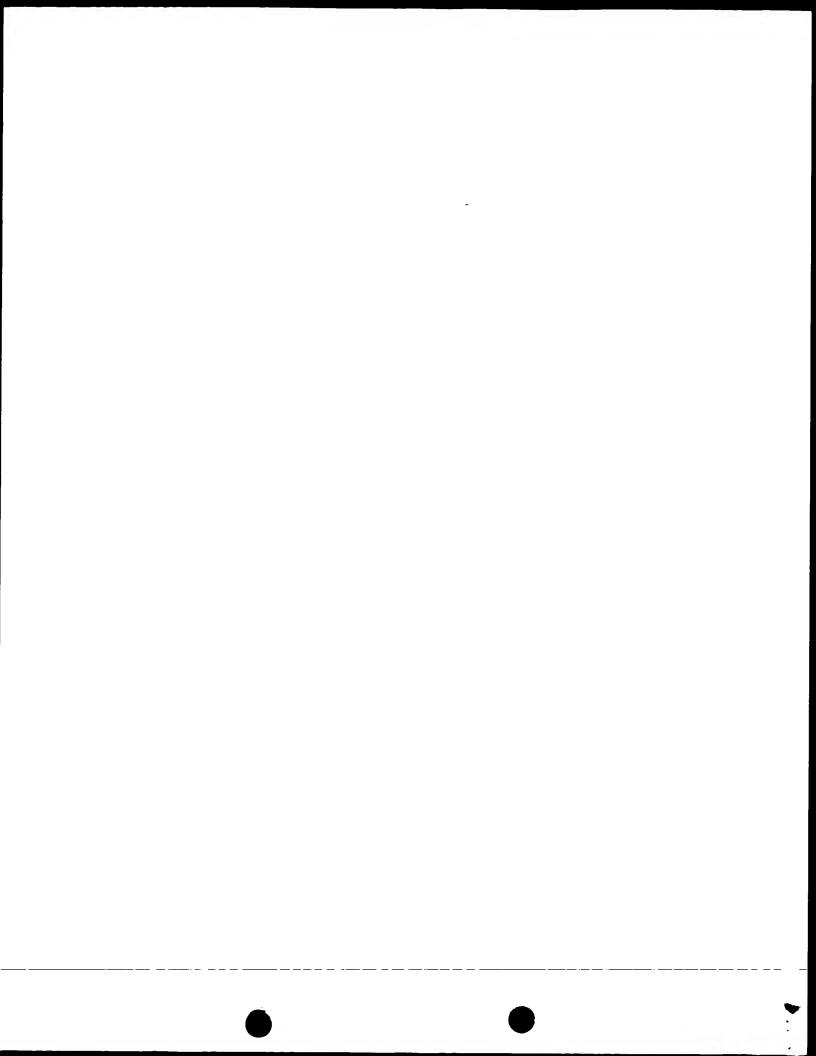
US-08-915-004-8.rst

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Homo sapiens
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1 (bases 1 to 442)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High qality sequence stops: 265
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                             #44 bp mRNA EST 16-MAR-1995 ye07c04.rl Homo sapiens cDNA clone 117030 5' similar to gb:x54486_rnal PLASMA PROTEASE C1 INHIBITOR PRECURSOR (HUMAN); 771938
IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS N21157 453 bp mRNA EST 19-DEC-1995 DEFINITION yx47d01.s1 Homo sapiens CDNA clone 264865 3' similar to
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 1.22e-05;
0; Mismatches 8; Indels
                                                                                                                                     Query Match 1.9%; Score 22; DB 6; Length 410; Best Local Similarity 80.6%; Pred. No. 2.66e-04; Matches 29; Conservative 0; Mismatches 7; Indels
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/clone="117030"
117 c 96 q 108
                                                 /organism="Homo sapiens"
/clone="85063"
57 c 83 g 124
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Best Local Similarity 79.5%;
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
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Fax: 314 286 1810
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Deuterosticmia: Chordata; Vertebzata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tertapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Rucaha,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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SP:TCPB_MOUSE P80314 T-COMPLEX PROTEIN 1, BETA SUBUNIT
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Release 2 Copyright D	.1D John F. Collins, Biocomputing Research Unit. (c) 1993, 1994, 1995 University of Edinburgh, U.K. istribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a. r Run on: Tu	n.a. database search, using Smith-Waterman algue Dec 2 15:51:34 1997; MasPar time 325.28 Sec
ular output not	generated.
Intle: >Us Description: (1) Perfect Score: 111 N.A. Sequence: Comp:	US-08-915-004-8 1-1185) from US08915004.seq 185 1 ATGAACAACTTGCTGTGCTGTAAAAATAAGCTGCTTATAA 1185 TACTTGTTGAACGACACGACATTTTATTCGACGAATATT
Scoring table: TA	TABLE default Gap 6
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tabase:	46:STS11 47:STS12 48:STS13  57-STS-FOUR 49:qneST1 50:qneST2 51:qneST3 52:qneST4 55:qneST1 65:qneST1 56:qneST3 57:qneST3 59:qneST1 66:qneST1 66:qneST1 76:qneST3 67:qneST3 62:qneST1 76:qneST1 76:qneST1 76:qneST2 71:qneST2 71:qneST2 71:qneST2 71:qneST2 71:qneST2 72:qneST3 72:qneST3 72:qneST3 80:qneST1 76:qneST2 72:qneST3 72:qneST3 72:qneST3 72:qneST3 72:qneST3 72:qneST3 72:qneST3 72:qneST3 72:qneST3 72:qneST3 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qneST2 72:qne
Statistics: Me	n 11.2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result

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1.110e+100

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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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WashU-Merck EST Project
Washington University School of Medicine
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/note-"Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHDU, and fetal heart NbHHJ9W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares NhHMPu S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                         Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 448.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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06-MAR-1997 (Rel. 51, Last updated, Version 1)
2r47g08.rl Soares NhHMPu S1 Homo sapiens cDNA clone 666590 5'.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertębrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 1; Indels
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Best Local Similarity 99.6%;
Matches 256; Conservative
                       Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.
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/note="Organ: mixed (see below); Vector: pt7t3D-Pac (Pharmacia) with a modified polylinker; Site_i: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHW, pregnant uterus NbHPV, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction
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        LOCUS
        AA195113
        530 bp
        mRNA
        EST
        17-JAN-1997

        DEFINITION
        Z7353003.rl
        Soares NhHMPu S1 Homo sapiens cDNA clone 665356 5.

        ACCESSION
        AA195113

        NID
        91784803

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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Lew,, Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                        Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This Clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for quality sequence stop: 448.
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Pred. No. 0.00e+00;
0; Mismatches 1; Indels (
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WashU-Merck EST Project";
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Best Local Similarity 99.6%;
Matches 256; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. High quality sequence stop: 257.
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2135a03.rl Soares NhHMPu S1 Homo sapiens CDNA clone 665356 5'
AA195113
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                              Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 530;
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Pred. No. 1.10e-102;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 74; Conservative
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                                                              Contact: Wilson RK
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/organ:micro saprate holds: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Equal amounts of plasmid DnA from three normalized libraries (melanocyte ZNNHW, pregnant uterus NDHPU, and fetal heart NDHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5.000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260132-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus" /lab_host="DH108"
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 257.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1112 ACAAATTGTATCAGAAGTTATTTTAGAAATGATAGGTAACCAGGTCCAATCAGTAAAAA 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 acaaattgtatcagaagttatttttagaaatgataggtaaccaggtccaatcagtaaaaa 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Putative full length read Seq primer: ETPrimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-APR-1996 (Rel. 47, Created)
23-ARR-1997 (Rel. 51, Last updated, Version 2)
ma38f10.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 313003 5'
similar to gb:219554 VIMENTIN (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Galsel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptce M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 74; DB 54; Lour Pred. No. 1.10e-102; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares NhHMPu S1"
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                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; RNA; EST; 267 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 g
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Matches 74; Conservative
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MqC12:
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          Buffer:
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BASE COUNT
                                                                                                                                                    source
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                                                                                                                                                                                   SIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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                                                                                                                                FEATURES
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STS sequence; primer; sequence tagged site. human Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 12 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institue for Medical Research, Canden, NJ 08103.
                                                                                                                                         normalization to a cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopteryg11; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 degrees C for 15 seconds 62 degrees C for 23 seconds 72 degrees C for 30 seconds 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 147259689
                                                                                                                                                                                                                                                                                                                                  Score 22; DB 95; Length 267;
Pred. No. 2.15e-04;
0; Mismatches 11; Indels
                                                                                                                                                                                                              /clone="313003"

/clone_lib="soares mouse p3NMF19.5"

/dev_stage="19.5 dpc total fetus"

/lab_host="DH10B (amplcillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                          gaagctgctggaaggcgaggagagcatgatttctctgcctctgc 74
                                                                                                                                                                                             Minoru Ko (Wayne State University)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIS
                                                                                                                                                                                                                                                                                                 Sequence 267 BP; 78 A; 70 C; 61 G; 58 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 ng
each 1 uM
each 200 uM
: 0.05 units/ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G10922 400 bp DNA
human STS SHGC-13782 clone pG-6721.
G10922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer A: GTAACCTCAAGAAAGCACCCC
Primer B: TGGTGGGGAGTATCAGGTTC
STS size: 98
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Richard M. Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Annealing:
Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taq Polymerase:
Total Vol:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Denaturation:
                                                                                                                                                                                                                                                                                                                                  Luery Match
Best Local Similarity 75.0%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR Cycles:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Template:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer:
dNTPs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9988028
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                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                     31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OURNAL
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RESULT

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SOURCE

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 450)
Gerken,S.C., Matsunani,N., Lawrence,E., Carlson,M., Moore,M., Ballard,L., Melis,R., Robertson,M., Bradley,P., Elsner,T., Tingey,A., Rodriguez,P., Albertsen,H., Lalouel,J.-M. and White,R. Sequence tagged sites from the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted by: Utah Center for Human Genome Research University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer; STS sequence; microsatellite marker; microsatellite
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                                                                                                                                                              Length 400;
                                                                                                                                                                                                                                                                                                                                       Score 22; DB 39; Length 400;
Pred. No. 2.15e-04;
....matches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat; repeat polymorphism; sequence tagged site.
Homo sapiens DNA.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gel: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
211 Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: TTGGGCTCCTTCTGGCAG
Primer B: GGCAAATGCCTTTGCATGC
Primer B: GGCAAATGCCTTTGCATGC
Primer B: GGCAAATGCTTTGCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            605 AACCTGAAGAATGCCTCCTCACACAGGGTAACAT 572
                                                                                                                                                                                                                                                                                                  111 t
                                                                                                                                                                                                                                                                                                                                                                                                                                     232 aacctcaagaaagcaccccacacagggtaaaat 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name="STS UT1054"
                                                                                                                                                           organism="Homo sapiens"
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230..437
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  필필필
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230..250
/map="12"
complement(308..327)
/map="12"
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complement(418..437)
                                                                                                                      Location/Qualifiers
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2.5
50
20
8.3
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Annealing: 60C 10sec
Extension: 72C 20sec
                                                                                                 Chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMUT1054 450 bp
Human STS UT1054.
L17757
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Best Local Similarity 82.4%;
Matches 28; Conservative
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                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Physiol. 106:1241-1255(1994).
AGIS: #42477; AGIS July 1995.
Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University MSU-DOE-PRL, Michigan State University, Plant Blology Bldg., E. Lansing, MI Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@ibm.cl.msu.edu. NCBI gi: 933235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
                                                                   372 acagagagagtnagnnggagagagaagannnanagataggaataaaagcatgcaaa 426
                                                                                                     W10113;
q1284430
29-ARR-1996 (Rel. 47, Created)
05-MAR-1997 (Rel. 51, Last updated, Version 2)
ma42d03.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 313349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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   Score 22; DB 48; Length 450;
Pred. No. 2.15e-04;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 472;
                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliopsida: Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                         02-FEB-1995 (Rel. 42, Created)
12-MAR-1997 (Rel. 51, Last updated, Version 15)
5740 Arabidopsis thaliana cDNA clone 113K15T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22; DB 77; 1
Pred. No. 2.15e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="var columbia"
/note="thale cress"
                                                                                                                                                                            standard; RNA; EST; 472 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="113K15T7"
Best Local Similarity 63.6%;
Matches 35: Concerns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 68.6%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..472
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 95148729.
                                                                                                                                                        LT 8
AT4774
T42477;
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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mp53f02.rl Soares 2NbMT Mus musculus cDNA clone 572955 5'.
AA117046
                               Unpublished.

Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of MedicineP 4444 Forest Park Parkway. WashIngton University School of MedicineP 4444 Forest Park Parkway. Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Putative full length
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Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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/clone="313349"
/clone=libe="Soares mouse p3NMF19.5"
/dev_statge="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA <1..5105
Sequence 105 BP; 57 A; 13 C; 21 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
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Pred. No. 3.88e-03;
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                "The WashU-HHMI Mouse EST Project";
                                                                                                                                                          read Seg primer: mob.REGA+ET.
Key Location/Qualifiers
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Best Local Similarity 76.9%;
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 Waterston R.;
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Putative full length read vector to vector length is 108 Seq primer: -28M3 rev2 from Amersham. Location/Qualifiers
                                                                              /clone_lib="Soares 2NbMT"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
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                                                                   /clone="572955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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Duboque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morits M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
Waterston R.,
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Vertębrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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18-F¢B-1997 (Rel. 51, Last updated, Version 2)
mp53‡02.rl Soares 2NbMT Mus musculus cDNA clone 572955 5'
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Pred. No. 3.88e-03;
vector to vector length is 108 seq primer: -28M13 rev2 from Amersham.
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                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMAA17046 standard; RNA; EST; 107 BP
                                                                                                                                                                                                                                                  /dev_stage="4 weeks"
/lab_host="DH10B"
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                           Location/Qualifiers
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                                                                     /strain="C57BL/6J
                                                                                                                                                                                                             572955"
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Best Local Similarity 76.9%;
Matches 30; Conservative
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q1672122
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by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructedby Bento Soares and M.Fatima Bonaldo."
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
and Eco RI sites of the modified pT7T3 vector. RNA provide
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                    Length 107;
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                                                                                                                                                                                                              /Lissue_type="Thymus"
/dev_stage="4 weeks"
/dab_host="DH10B"
mRNA
<1..>107
Sequence 107 BP; 50 A; 16 C; 24 G; 17 T; 0 other;
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SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygli; Choanata;
Petrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prepared with primer pairs derived from random genomic sequence. Location/Qualifiers
                                                                                                                                                                                                         Whitehead Institute/MIT Center for Genome Research; Physically
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/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;
963_G_6"
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                                                                                                                                                                                                                                                                              Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
191: 617 252 1900
Fax: 617 252 1902
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STS sequence; primer; sequence tagged site.
human STSs derived from random genomic DNA.
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Best Local Similarity 70.8%; Pred. No. 3.88e-03;
Matches 34; Conservative 0; Mismatches 14;
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dNTPs: each 4 nM
Taq Polymerase: 0.025 units/ul
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                                                                                                                                                                                                                                                                                                                                                                                          Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer B: AAAGGAGTCAAAATGGGTTTTT
STS size: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Denaturation:
Annealing: 56 degrees C
Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 g
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Thermal Cycler:
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KCl: 50 mM
Tris-HCL: 10 mM
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PCR Profile:
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Eukaryotae; mitochondrial eukaryotes; Catarrhini; Hominidae; Homo.

I (bases it or 194)

Gerken,S.C., Matsunami,N., Lawrence,E., Carlson,M., Moore,M.,
Ballard,L., Mells,R., Robertson,M., Bradley,P., Elsner,T.,
Tingey,A., Rodriguez,P., Albertsen,H., Lalouel,J.-M. and White,R.
Genetic and physical mapping of simple sequence repeat containing
sequence tagged sites from the human genome
Unpublished (1993)

Submitted by: Utah Center for Human Genome Research University of
Utah, Dept. of Human Genetics
Salt Lake City, UT 84112

E-mail: sts@corona.med.utah.edu
Primer A: CTACTOAGGAGGAGAGA
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Homo sapiens DNA.
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                                                                                                                                                                     Gaps
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Pred. No. 3.88e-03;
0; Mismatches 15; Indels
                                                                                                                      STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mg++: 1mM
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial Denaturation: 94C 300sec
PCR Cycles: 5
Benaturation: 94C 10sec
Annealing: 58C 10sec
Extension: 72C 20sec
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
<1..>107
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Human STS UT5145.
L17708
g308208
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Best Local Similarity 70.0%;
Matches 35; Conservative
                                                                                                                           Query Match 1.8%;
Best Local Similarity 76.9%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32P-label: A Primer PCR Profile:
                                                                        16 c
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Gaps

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primer_bind primer_bind

STS

ATURES

BASE COUNT

RESULT 14

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Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; mitochondria; Osteichthyes; Sarcopterygii; Choanata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.

1 (bases 1 to 253)
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/map="923_H_8; 959_F_5; 441.7 cR from top of Chr17 linkage
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/map="923_H_8; 959_F_5; 441.7 cR from top of Chrl7 linkage
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                                                        STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
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Pred. No. 3.88e-03;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                       Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
FIL: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu
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Primer: each 5 pM
dNTPs: each 4 nM
Tag Polymerse: 0.025 units/ul
Total Vol: 20 ul
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Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
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Best Local Similarity 78.4%;
Matches 29; Conservative
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KC1: 50 mM
Tris-HCL: 10 mM
pH: 9.3
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  human STS WI-6406
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DEFINITION
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                                                                                                                                                                                                                        REFERENCE
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                                                        KEYWORDS
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Search completed: Tue Dec 2 16:04:01 1997 Job time: 747 secs.

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MPsrch_nn n.a n.a.	rch, using Smith-Wate
Run on: Tue Dec	2 16:04:23 1997; MasPar time 910.66 Seconds
bular output not generated	1313.360 Million .
111e:	915-004-10 ) from US08915004.seq ATGAACAAGTTGCTGTGCTGTAAAAATAAGCTGCTTATAA 1089 TACTTGTTCAACGACACGACATTTTTATTCGACGAAATAT
Scoring table: TABLE defi Gap 6	fault
Nmatch STD : Dbase 0;	Query 0
Searched: 362067 se	eqs, 549138275 bases x 2
Post-processing: Minimum Post-processing:	Match 0% first 45 summaries
Database: embl-new3 1:BCT 2 9:ORG 1	13 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:INC
17:VIR Database: genbank99 18:BCT7 25:BCT7	9 1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7 8 26:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2
31:GEN3 3 38:INV4 3 45:INV11 52:VRT4 5 59:PKT4 5	3 32:HTG1 33:HTG2 34:HTG3 35:INV1 36:INV2 37:INV3 4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10 14 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT 51:VRT3 4 53:PRT1 54:PRT2 55:PRT3 56:PRT4 57:PRT5 58:PRC 160:PLM2 61:PLM3 62:PLM4, 63:PLM5 64:PLM5 65:PLM7
66:PLN8 6 72:PRI3 7 79:PRI10 85:ROD1 8	N8 67:PLN9 68:PLN10 69:PLN11 70:PRI1 71:PRI2  I3 73:PRI4 74:PRI5 75:PRI6 76:PRI7 77:PRI8 78:PRI9  I10 80:PRI11 81:PRI12 82:PRI13 83:PRI14 84:PRI15  B 68:ROD2 87:ROD3 88:ROD4 89:ROD5 90:ROD5 91:ROD7
99:NDG 99 99:NRL4 10 105:VRL4 0 105:VRL4 9enbank-new3	0 55:51K 54:51K 55:UNA 56:VKL1 57:VKL2 58:VKL3 4 100:VRL5 101:VRL6 102:VRL7 103:VRL8 104:VRL9 L10 new3
11	T 107:CEN1 108:GEN2 109:HTG1 110:HTG2 111:INV H 113:VFT 114:PHG 115:PLN 116:PR11 117:PR12 D 119:SYN 120:UNA 121:VFL
Database: u-embl50_99 122:part	99 t1
Statistics: Mean 11.	.131; Variance 4.282; scale 2.599
Pred. No. is the numb score greater than or and is derived by ana	number of results predicted by chance to have a n or equal to the score of the result being printed, analysis of the total score distribution.

SUMMARIES

Pred. N	ten 4.40e ten 1.20e 57kb 1.20	37kD 1.33e	uence ** 5.89e PA gene, 2.50	A gene, 2.50e nitrogen 2.50e RNA for 2.50e	tis elegan 2.50e+00 es cerevis 2.50e+00 equence ** 2.50e+00	lax 57kD 1.01e 1lax 57kD 1.01 phospho 1.01e	interleu 1.01e nor necr 1.01e	necr 1.01	gen 1.01e aten 1.01e -ket 1.01e	ene. 1.01e osis 1.01e	egan 1.01e use 1.01e	ass 1.01e	egan 1.01e F42 1.01e	noso 1.01e	ile 1.01e+01	stomatitis 3.85	etoplast m 3.85e+01	sequence fr		30-0CT-1996		totz,H. es and their use to		, , , , , , , , , , , , , , , , , , ,
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1 (bases 1 to 354)

Dook, T.G., Doerder, F.P., Jahn, C.L. and Herrick, G. A proposed superfamily of transposase genes: transposon-like
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Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use tecntrol fungal disease
Fatent: US 5569830-A 5 29-OCT-1996;
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Query Match 2.8%; Score 30; DB 57; Length 215; Best Local Similarity 13.3%; Pred. No. 4.40e-05; Matches 26; Conservative 80; Mismatches 86; Indels
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Pred. No. 1.20e-03;
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Witherspoon,D.J., Doak,T.G., Williams,K., Seger,J. and Herrick,G. Selection on the protein-coding genes of the TBE1 family of transposable elements in the ciliates Oxytricha fallax and O.
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Doak T.G., Williams, K., Witherspoon, D.J. and Herrick, G.
Direct Submission
Submitted (11-FEB-1997) Oncological Science, University of Utah, School of Med. Rm5C334, USA, UI 84132, USA
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/note="this is a bulk sequence that was generated from PCR product that represents many transposon templates"
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13-WAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein chimera gene, partial
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elements in ciliated protozoa and a common 'D35E' motif
Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
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"A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common 'D35E' motif";
Proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
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hypotrichs; Stichotrichida; Oxytrichidae; Oxytricha.
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/db_xref="PID:g1881676"
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Pred. No. 1.20e-03;
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Oncological Science, University of Utah, School of Med. Rm5C334,
USA, UT 84132, USA
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13-WAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein chimera gene, partial
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/product="57kD zinc finger/protein chimera"
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Pred. No. 1,33e-01;
38; Mismatches 36;
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Best Local Similarity 23.7%;
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/translation="HTRDLXKHLLKAHKKXXEXEXXXXXLKXLXKRRAREXXXXXXX
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3 (bases 1 to 354)
3 (bases 1 to 354)
Doak_T.G., Williams, K., Witherspoon, D.J. and Herrick, G.
Direct Submission
Submitted (11-FEB-1997) Oncological Science, University of Utah, School of Med. Rm5C334, USA, UT 84132, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          /note="this is a bulk sequence that was generated from PCR product that represents many transposon templates"
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A proposed superfamily of transposaes genes: transposan-like
elements in ciliated protozoa and a common 'D35E' motif
Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryotae; mitochondrial eukaryotes; Alveolata; Cillophora;
hypotrichs; Stichotrichida; Oxytricha.
1 (bases 1 to 354)
                                                           Submitted (11-FEB-1997) to the EMBL/GenBank/DDBJ databases.
Oncological Science, University of Utah, School of Med. Rm5C334,
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/transi_table=6
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   Doak T.G., Williams K., Witherspoon D.J., Herrick G.;
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Seguence 354 BP; 106 A; 42 C; 41 G; 54 T; 111 other;
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/strain="9D1"
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Oxytricha fallax
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USA, UT 84132, USA
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H.sapiens LIPA gene, exon
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2 (bases 1 to 1851)
Aslanidis, C.
                                                                                                      Direct Submission
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Submitted (07-AUG-1991) G. Wiche, Inst of Biochemistry, University
of Vienna, Waehringerstrasse 17, 1090 Vienna, AUSTRIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                                                                                                                                                            rgcdagrgaryhhyhdwargwbgydgwgcyykaayaagcwagmgarwyaswrtrygtaar 158
                                                                                                                                                                                      RRMAPIB5 7095 bp RNA ROD 21-0CT-1992 R.norvegicus mRNA for microtubule associated protein IB. X60370 X60371 X60550
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1 (bases I to 7095)
2 uner, W., Kratz., Staunton, J., Feick, P. and Wiche, G.
Identification of two distinct microtubule binding domains on
                                                                                                                     0; Gaps
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Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
799F10; HTGS phase 1.
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                                                                              Length 354;
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Pred. No. 1.33e-01;
38; Mismatches 36; Indels
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Best Local Similarity 76.1%; Pred. No. 5.89e-01;
Matches 35; Conservative 0; Mismatches 11; Indels
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               HQYAYKVYPFNYLX"
Sequence 354 BP; 106 A; 42 C; 41 G; 54 T; 111 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant rat MAP 1B
Eur. J. Cell Biol. 57 (1), 66-74 (1992)
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1856 c 1799 g 1316 t
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/tissue_type="brain"
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Best Local Similarity 23.7%;
Matches 23; Conservative
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Rattus norvegicus
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HTG; HTGS_PHASE1.
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TITLE JOURNAL

MEDLINE REFERENCE

AUTHORS

JOURNAL

AUTHORS REFERENCE

TITLE

source

TURES

TITLE JOURNAL

REFERENCE AUTHORS

REMARK

BASE COUNT

DEFINITION

RESULT

g οy ACCESSION

KEYWORDS

SOURCE

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with foreign sequence from B.coli, yeast, vector, phage etc. Order of segments is not known: 800 n's separate segments. Unfinished sequence: BK799F10 Contig_LD: 00051 Length: 885 bp Unfinished sequence: BK799F10 Contig_LD: 00064 Length: 885 bp Unfinished sequence: BK799F10 Contig_LD: 00185 Length: 830 bp Unfinished sequence: BK799F10 Contig_LD: 00185 Length: 830 bp Unfinished sequence: BK799F10 Contig_LD: 00963 Length: 958 bp Unfinished sequence: BK799F10 Contig_LD: 00968 Length: 958 bp Unfinished sequence: BK799F10 Contig_LD: 00968 Length: 958 bp Unfinished sequence: BK799F10 Contig_LD: 0156 Length: 958 bp Unfinished sequence: BK799F10 Contig_LD: 0156 Length: 13742 bp Unfinished sequence: BK799F10 Contig_LD: 02185 Length: 13742 bp Unfinished sequence: BK799F10 Contig_LD: 02223 Length: 1000 bp Unfinished sequence: BK799F10 Contig_LD: 02223 Length: 1000 bp Unfinished sequence: BK799F10 Contig_LD: 02224 Length: 1314 bp Unfinished sequence: BK799F10 Contig_LD: 02225 Length: 1341 bp Unfinished sequence: BK799F10 Contig_LD: 02225 Length: 1341 bp Unfinished sequence: BK799F10 Contig_LD: 02225 Length: 1361 bp Unfinished sequence: BK799F10 Contig_LD: 02225 Length: 13670 bp. (finished sequence: BK799F10 Contig_LD: 02214 Length: 13670 bp. (finished sequence: BK799F10 Contig_LD: 02214 Length: 13670 bp. (finished sequence: BK799F10 Contig_LD: 02214 Length: 13670 bp. (finished sequence: BK799F10 Contig_LD: 02214 Length: 13670 bp. (finished sequence: BK799F10 Contig_LD: 02214 Length: 13670 bp. (finished sequence: BK799F10 Contig_LD: 02214 Length: 13670 bp. (finished sequence: BK799F10 Contig_LD: 02214 Length: 13670 bp. (finished sequence: BK799F10 Contig_LD: 02214 Length: 13670 bp. (finished sequence: BK799F10 Contig_LD: 02214 Length: 13670 bp. (finished sequence: BK799F10 
                                                                                                                                                                                                                                                                                             Submitted (06-NOV-1996) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests. clonerequest@sanger.ac.uk IMPORTANT: This sequence is unfaished and does not necessarily represent the correct sequence. Work on the sequence is in progress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1851)
Aslanidis, C., Klima, H., Lackner, K.J. and Schmitz, G.
Genomic organization of the human lysosomal acid lipase gene (LIPA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid cholesteryl ester hydrolase; lipA gene; lysosomal acid lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated
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                                                                  Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 115419)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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Gaps

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NEEDIAFASGLNGGTFDSMLEALPDDLYFTDFVSPFTAAATTSVTTKTVKDTTPATNH
MDDDIAMFDSLATTQPIDIAASNQQNGEIAQLMDFNVDQFNMTPSNSSGSATISAPNS
FTSDIPQYNHGSLGNSVSKSSLFPYNSSTSNSNINQPSINNNSNTNAQSHHSFNIYKL
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LANFKRAASVSSISNMEPSGONKKPLIQCFNCKTFKTPLWRRSPEGNTLCNACGLFO
KLHGTMRPLSLKSDVIKKRISKKRAKQTDPNIAQNTPSAPATASTSVTTTNAKPIRSR
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FNGASNANLLNSNNLARHNSNTVYGNFRRSSRRSSTSSNTSSSSKSSSRSVPILLPKPS
PNSANGQOFRNNNLANTNNYSAGNSTSSRTSSNTSNSPLOQNLLSNSFORO
GMNIPRRKMSRNASYSSPLOQUHEQOOVDVNSNTNTNSNSPLOQNLSNSFORO
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LSSDYYGOKPNPDIFNTPVDSFSSRSKSHTSLLSQOLONSESNNFISNHKFNNR
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                                                                                                                                         YSCGLN3 3021 bp DNA PLN 15-SEP-1990
S.cerevislae nitrogen regulatory protein (GLN3) gene, complete cds.
M35267
                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 3021)
Minehart, P.L. and Magasanik, B.
Sequence and expression of GLN3, a positive nitrogen regulatory
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                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1990)
Draft entry and computer-readable [or printed] sequence for [1]
kindly submitted by P.Minehart, 19-JUN-1990.
Author address: P.Minehart
                                                                                                                                                                                                                                nitrogen regulatory protein.
S.cerevisiae (strain S288C) DNA.
Saccharomyces cerevisiae
Saccharomyces cerevisiae
Eukaryotae; mitochondrial eukaryotes; Fungi; Ascomycota;
Hemlascomycetes; Saccharomycetaceae;
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Pred. No. 2.50e+00;
0; Mismatches 12; Indels
       9; Indels
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/organism="Saccharomyces cerevisiae"
1..140
                                           region"
       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="GLN3"
/note="acidic activation
/db_xref="SGD:L0000710"
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730..2922
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Location/Qualifiers
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Best Local Similarity 74.5%;
Matches 35; Conservative
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       32; Conservative
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Direct Submission
Submitted (02-NOV-1993) C. Aslanidis, Inst for Clinical Chemistry &
Lab. Med., University of Regensburg, 93042 Regensburg, FRG
Location/Qualifiers
1..1851
/organism="Homo sapiens"
/clone_lib="human placenta DNA cloned in lambda FIXII
(stratagene)"
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1851)
Aslanidis,C., Klima, H., Lackner,K.J. and Schmitz,G.
Genomic organization of the human lysosomal acid lipase gene (LIPA)
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Submitted (02-NOV-1993) C. Aslanidis, Inst for Clinical Chemistry & Lab. Med., University of Regensburg, 93042 Regensburg, FRG
Lab. McCation/Qualifiers
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acid cholesteryl ester hydrolase; lipA gene; lysosomal acid lipase.
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/clone_lib="human placenta DNA cloned in lambda FIXII
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Pred. No. 2.50e+00;
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Pred. No. 2.50e+00;
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<1..948
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1138..>1851
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1138..>1851
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H.sapiens LIPA gene, exon 4.
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949..1137
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Aslanidis, C.
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Best Local Similarity 78.0%;
                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 2.1%;
Best Local Similarity 78.0%;
atches 32; Conservative
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The 5' end lies in a gap followed by the cosmid ZK1248:3' cosmid is F59G1, 200 bp overlap. Actual start of this cosmid is at base position 1 of CELF55C12; actual end is at base position.
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/translation="WVGASLLQSDDDSDVPDLDLRGASSSSRRRNFFSKSTADYEE1
RHRQKTYKTIFLFSFIFIFLLALYFLYNAMCRLKLLSDEIDDLRQKMGHVEEFQLELK
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//translation="WHNEFSAVLFTILIISIDGAINCFYGIEETAPGVHISNIVKT
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110830..11285,11330..11492,11541..12262,12310..12831,
12877..12999,13088..13144,13830..13847))
/gene="F55G12.5"
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Department of Genetics, Washington University,
Department of Genetics, Washington University,
ST. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
e-mail: rw@nematcde.wustl.edu and jes@sanger.ac.uk
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/evidence=not_experimental
/gene="F55C12.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of C. elegans cosmid F55C12 Unpublished (1995) 3 (bases 1 to 38586)
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/gene="F55C12.3"
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94150718
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Direct Submission
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ANALGVENVGGIFVVLLVGLALAVIVAIIEFIYKSKENAYEDKQSLCNEMAEELRFAI
RCTGASKRPKNKFKSRCQDCREGKPHSSHSHHLQEIGPESPPNGIVQLRPTKKSPSAV
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Submitted (23-MAY-1995) M.G. Darlison, Inst. fuer Zellbiochemie &
Klinische, Neurobiologie, Universitaets-Krankenhaus Eppendorf,
Universitaet Hamburg, Martinistr. 52, 20246 Hamburg, FRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Darlison, M.G. Structure and pharmacological properties of a molluscan glutamate-gated cation channel and its likely role in feeding
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/db_xref="PID:e183756"
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Caenorhabditis elegans
Eukaryotae; mitcohondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Mollusca;
Gastropoda; Pulmonata; Basommatophora; Lymnaeidae; Lymnaea.
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Pred. No. 2.50e+00;
0; Mismatches 7; Indels
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96194572
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U41107
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/clone_lib="lambdazAPII"
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                                                                                                      glutamate receptor .
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Stuhmer, T., Amar, M.,
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Best Local Similarity 81.1%;
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Dietrich, F.
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YRGWINELRTRYSPANYHVUSSGSVLVRLEGSMLRICRPARAYLKHAFYDDPTLKQNO
PSMVSQVI YDMKDATYFRLARRENWSRKYPIHIRFAHSSSLVELDHSSKAKSR
GMSRGASMAPHPNISTSTSEGRRHSVEDBETTOSTAEGSBEVEDERKKNYRANGSDIO
EFRESNSHKKRGRSIYLFVRAAREKERWFHLLREACARARNSPKVRRCMSVIVKTCSS
                                                                                                                                                                                                                                                                                    ASLPEEIFRGEDDATNTSVAVDALAAEKEDFSESMFNSPKRICLPKEYETLKYRSNYA
SEVRQLATILLSIQVPRREENSTYSVDUGTMWRAPGAQOISTELDOS FNYLARIFFD
FCRDDFWIRDYKQKILOSKLATITLPYFIEKLELGELKEGTAAPKFTYYTPKYDEWGT
WYDFEMKYKGGIRLVLOTSINLLKLQSGSHQVKTEKRVNRWTESVRYTRYSDEDLFES
PESSPEDEFGAKNNSEGTYKEKTGKKILISIVERAAQSSLERGKAKLQAVARLIEDVST
PLEMLAVEVEEVEGYARNTONIPPPPSDRLWYAFRRFILKLRAVPQVGDRSVDLSTVSE
WIETKLRQVLEKNLVCPMMDDIILPVLSGNPLLHMGYNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/db_xref="PID:g1086795"
/db_xref="PID:g1086795"
/tbanslation="Margiffkiamilkfkilponhiirgisskinkissnlddydydyn PDbnlefevfwdeogangfffkiaestsfwrsswgdarffeciillkgfesiaysfhtigy KSLGLOPDFRHIGMAWPEKRGKSILKVYTPYLIQBERMKHQNMLACNYHWSONFWL KATGRSDIGACTYXISYYELYDFKVPIPKINDDCEIVVKNVNTKTVTDVLKYDTSIFP
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SMLEEVIEKNKKIRRFQVRSNDOCSNSYE"
19575...19691
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IADTPSLADELAGGDSSQLLDALREQEICNQKLRVYINGILMRVIERHPEILEIGEEG
ILSKLTVRRRISVLANVVVIIDSRRVIITDTFSKNLRLPSLIVSSMGMNRHMTSSTIG
                                         /translation="MSEMERVIINAVSRSRSRCRREKWLLPEHVIPAGGELQKSSTP
SGSVDDGEQKDKVSIGSNDSGKKESEQSKIGALLEKAKKKTHKLVSSRKKNHSECGTS
                                                                                                 DVSPHPSMRSLDSISKSEERIASRRSSGGSSDQLKQSKVPDNSNDESVEILEEIVAKR
TANQNLIDPADPSDPFLVQSFIHKCRVLPFFRARLVVFGSLIALTIACPGFITGLMMG
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RIRNELEKTENKLEEAQLLVEGMEEERIQLEROFRKFKEEAQQDIDSSSEMVEVLALE
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/translation="MRLQGSSASSASVASRLYGTRSRRDSLGGSSSESDLIAFGGDQD
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/ccdon_start=1
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join(32784..32939, 33175..33899, 33887..34065,34151..34515)
/evidence=not_experimental
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18255.1896,18925.18948))
Aevidence-anot, experimental
/gene="F55C12.6"
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Pred. No. 2.50e+00;
0; Mismatches 19; Indels 1; Gaps
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                   /db_xref="PID:91086794"
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Dietrich,F.S., Mulligan,J., Hennesy,K., Allen,E., Araujo,R.,
Aviles,E., Berno,A., Brennan,T., Carpenter.J., Chen,E.,
Aviles,E., Herno,A., Brennan,M., Guzman,E., Hartzell,G.,
Hunicke-Smith,S., Hyman,R., Kayser,A., Komp,C., Lashkari,D.,
Lew,H., Lin,D., Mosedale,D., Makahara,R., Namath,A., Norgen,R.,
Shogren,T., Smith,V., Taylor,P., Wei,Y., Yelton,M., Botstein,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISPONLEPAIRILNNKGKQQENIDDAEDGSSKKEHHYYKALALAKRRNROARIHSH
DDIINLGKASQMDMSLLAAAFSGNSTTINNDQSSNEQTDEKILDIERYTTSTLTSS
ETTSPINKSCFYSQTLSLSFKIRHDDLQSSPSKVKNKDSQNSTLNKKKVRISLNRKE
EEKYYSINNNSDEYSVNEKETHKANDCNDESSENGDGDDDDDDDDDDDDDES
EFSFEYYSINNNSDEYSVNEKETHKANDCNDESSENGDGDNDHDDYDDDDDDDDES
EFSFEYAGINVRISSVKYYKFNDLFNLSDDDEEDGRONDHDDNNCIEDDESGNSGNEI
CGLGTRFEETSLKSNKVKKFNDLFNLSDDDEEEDGKNNNNDENESDNLYQKRLENG
GLN3 (positive nitrogen regulatory protein); MEI4 (meiosis-specific gene); HOM3 (aspartate kinase); CAJ1 (dnaJ homolog); tRNA-Gln. baker's yeast strain-5288C (AB972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLQSSLYETKSESHPPNHPHSQILQTPAKIVITPSVSDAQSQALAITDDDGEDDDDDT
SSILRIPFQLIDSSHSQQPHYASPQYTAVLNSPPLPPPARSQSLKYHDLNCDLDSEVP
RPMSNLFFIDEAEEDEYNQKSKFFDFDHYDIDĖINGIPEDFNFSDSERDDLNRRILKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="PID:9603266"
/translation="MRSFIKAHKKSTSFDESPKRHSNFSGNTNNSSQRSSDDSLDFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KETFNGNHGGHDDASLGETVDNKEQFLINDNVKKPIOKYNDLFDLSDEDDNDDKEMS
EAESYMFSDEAPSIESGPANAKSTRGIYSQSNKNIIRDGKPNYSFSLKRNNSDDETEH
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SNNWNTYDCNSLSRKTSSQMRDSKYQNHNVGQNVEPSSVLSPQHQISNGLDGKCNDNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISNSFVLONPPTKNTGPPPPLPPPLFPSSSTSSFSRHDNESEYTAYKKTSPAKDFNRT
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                                                                                                                                                                                                                                                                                                                     The sequence of S. cerevisiae cosmids 9379, 9581, and lambda clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neighboring Sequence:
The 5' end of this sequence overlays with GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete sequence of Saccharomyces cerevisiae chromosome V Unpublished (1994)
                                                                                                                                      Eukaryotaė; mitochondrial eukaryotes; Fungl; Ascomycota;
Hemiascomycetes; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted by: Stanford DNA Sequence & Technology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palo Alto, CA 94304, USA e-mail: dietrich@genome.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Saccharomyces cerevisiae"
/strain="S288c (AB972)"
/chromosome="V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Saccharomyces cerevisiae"
/clone="cosmid 9379"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence-not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain-"S288C (AB972)"
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/gene="YER033c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="cosmid 9581"
177..41762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                            Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-DEC-1994)
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Dietrich, F.S.
                                                                                                                                                                                                                    Saccharomyces.
1 (bases 1 to 43100)
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                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1994)
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/product-"Gln3p"
/db_xref-"PlD:g603273"
/db_xref-"PlD:g603273"
/translation-"MQDDPENSKLYDLLNSHLDVHGRSNEEPRQTGDSRSQSSGNTGE
NEEDIAFASGLNGGTFDSMLEALEDDLYFTDFVSPFTAAATTSVTTKKVKDTTPATNH
MDDDIAMFDSLAATTQPIDIAASNQONGEIAQLWDFNVDQFNMTPSNSSGSATISAPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LANFKRAASVSSISNMEPSGQNKKPLIQCFNCKTFKTPLWRRSPEGNTLCNACGLFO
KKLGCTMRPLSLKSDVIKRLSKRRKQTDPNIAQNTPSAPATASTSVTTURRPIRSR
KKLGQNSLSRVIPEEIIRNIGNTNILUNVNRGQYNFNSVPSPVLMNSQSYNSSNAN
FNGAKNANLNSNNLMRNSVTTPRFRSFRSSTSSNTSSSKSSRSVVPILPKPS
PNSANSQQFNMNLMTTNNVSAGNSVASSPRIISSANFNSNSPLQONLLSNSFQRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMNIPRRKMSRNASYSSSFWAASLQQLHEQQQVDVNSNTNTNSNRQNWNSSNSVSTNS
RSSNFVSQKPNFDIFNTPVDSPSVSRPSSRKSHTSLLSQQLQNSESNSFISNHKFNNR
LSSDSTSPIKYEADVSAGGKISEDNSTKGSSKESSAIADELDMLKFGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="PID:9603274"
/translation="MGVSQIWEFLKPYLQDSRIPLRKFVIDFNKSQKRAPRIAIDAYG
WLFECGFIQNIDISPRSRSRSRSPTRSPRDSDIDSSQEYYGSRSYTTTGKAVINFISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLLFFSVLLGADYNRGVKGLGKNKSLQLAQCEDPNFSMEFYDIFKDFNLEDLTSESLR
KSRYRLFQKRLYLYCKDHSVELFGRNYPVLLNQGSFEGWPSTVAIMHYFHPIVQPYFD
EEVLSDKYINMAGNGHYRNLNFNELKYFLQSINLPQISSFDKWFHDSMHEMFLLREFL
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                                                                                                          LTSFIMMVLSSVVATWGDQQAIAÎKASSLEDLDQELVESTIFVLNPGYLWMFTNCISS
ALFVLIMRKRIRLINFKDYDTWFYNNVLALPLLLVFSFIMEDWSTKNLSSVNLSADSLA
                                                                                                                                                                                      AMVISGLMSVGISYCSGWCVRVTSSTTYSMVGALNKLPIALAGLVFFDAPKNFLSFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTSDIPQYNHGSLGNSVSKSSLFPYNSSTSNSNINQPSINNNSNTNAQSHHSFNIYKL
QNNNSSSSAMNITNNNNSNNSNIQHPFLKKSDSIGLSSSNTTNSVRKNSLIKPMSSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKELLSLNVEFLLVFDGVMKPSFKRKFNHEQNATTCDDEKEYYSSWEQHVKNHEVYGN
CKGLLAPSDPEFISLVRKLLDLMNISYVIACGEGEAQCVWLQVSGAVDFILSNDSDTL
VFGGEKILKNYSKFYDDFGPSSITSHSPSRHHDSKESFVTVIDLPKINKVAGKKFDRL
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                                                                                                                                                                                                                                                                                                                                   /note="YER040w; positive nitrogen regulatory protein; contains putative zinc finger (GABA type) domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-1997
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Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
111J24; HTGS phase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to DNA repair protein Rad2p from S. cerevisiae, Swissprot Accession Number P07276" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 12932 aaaaaacctctgatacaatgtttcaattgtaaaaactttcaagacacc 12978
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Pred. No. 2.50e+00;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cp 1038 AAATAACTICTGATACAATTIGTACATTGTGAAGCTGTGAAGGAACC 992
                                                                                                                                                                                                                            IFLGFLSGLLYAVAKQKKIQQQKVLAATLEK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/product="Yer041p"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SGD:L0000710"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: remainder of annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="YER041w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 2.1%;
Local Similarity 74.5%;
les 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                              CDS
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                                                                                                                                                                                                                                                                                             TEBKDODOGOPALKSNEDRYYEDPYLEDPHGAVANABLNKVIKDVIKNRIQONDDATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLVSHSQDFINGVCTNMIDMRAQKLTAYGGNYDSYHKTRSELETNQMKOYNKQOEEIQ
HIKKEIASAGTYANIJWQAKSRQKILDKMEADGLVQPVVPDKVFSFREPQVERLPPPV
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VVSHDFRLLDKIAQDIFVVENKTATRWDGSILQYKNKLLAKNVVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWLFTNSYKNHAIRCVKILGIADLFDGITYCHYDRPIEEEFICKPDPKFFFTAKLQSG
LSSFANAWFIDDNESNVRSALSMGMGHVIHLIEDYQYESENIVTKDHKNKQQFSILKD
ILEIPLIMDVEVYRPSSIAIKEMEELEEEGGAVNWSNQQINVQSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTAYSFLFGSSRSQGKVPEFVHLKCPSITNLLVLFGVNQEKCNSLKINYEKKENSRYD
NLCTIFPVNKMLKFLMYFYSDDDNDDVRFFFLKAFICLILDRKVFNAMESDHRLCFKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAQHELKRIEDDVEKTILEDGPESELLEPLYERMDSLDPDFESRAAIILIGLGFNKK
TILKKTKDMSGGWKMRVALAKALFVKPTLLLLDDPTAHLDLEACVWLEEYLKRFDRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="PID:g603270"
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BYGLSVKGLIKNKQIDDVLQYNTFIDDSLPLQDYLKPDWKLRELLINLKKKKLGKFDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHPNFISDPENDSLNSDEEFSSLENSDLNLSGAKAESGDDFDFILKRTIISKRKAPSN
NEDEEIVKTPRKLVNYVPLKIFNLGDSFDDTITTTVAKLQDLKKEILDSPRSNKSIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSNTVAKSELQKSIKFSGSIPEIYLDVVTKETISDKYKDWHFISKNCHYEQLMDLEMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to hypothetical protein F42A10.1 from Caenorhabditis elegans, GenBank Accession Number U10414; contains motifs typical of ABC transporter proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
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VISPNLPTTITPTNSFTKPTPEFSNDYSLSPIQETPSSVQSSPKRA"
                                                                                                                                                    /evidence=not_experimental
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                                                                                                                                                                                      /product="Yer034p
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                                         4086,.4643
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With foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished sequence: dJil1374 Contig_ID: 00116 Length: 18287 by Unfinished sequence: dJil1374 Contig_ID: 00244 Length: 13962 by Unfinished sequence: dJil1374 Contig_ID: 00294 Length: 10666 by Unfinished sequence: dJil1374 Contig_ID: 00231 Length: 794 by Unfinished sequence: dJil1374 Contig_ID: 00031 Length: 794 by Unfinished sequence: dJil1374 Contig_ID: 01907 Length: 794 by Unfinished sequence: dJil1374 Contig_ID: 01907 Length: 4036 by Unfinished sequence: dJil1374 Contig_ID: 01907 Length: 5939 by Unfinished sequence: dJil1374 Contig_ID: 01907 Length: 558 by Unfinished sequence: dJil1374 Contig_ID: 02681 Length: 558 by Unfinished sequence: dJil1374 Contig_ID: 02187 Length: 5188 by Unfinished sequence: dJil1374 Contig_ID: 02187 Length: 5188 by Unfinished sequence: dJil1374 Contig_ID: 02187 Length: 3188 by Unfinished sequence: dJil1374 Contig_ID: 02187 Length: 3188 by Unfinished sequence: dJil1374 Contig_ID: 02255 Length: 1173 by Unfinished sequence: dJil1374 Contig_ID: 02255 Length: 21019 by.
Buck,D.

Direct Submission
Submitted (06-NOV-1996) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CBIO 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and
                                                                                                                                                                                                                                                                                                                    the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * This sequence is unfinished. When sequencing is complete,
    the sequence data presented in this record will be replaced
    *by a single finished sequence with the same accession number.
    Location/Qualifiers
    1.14576
    /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *** WARNING: Phase 1 High Throughout Genome Sequence ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="22"
36917 a 31170 c 31921 g 33145 t 12597 others
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ORIGIN
    AUTHORS
TITLE
JOURNAL
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Db 82692 gaaacaacaaaacaaagaccaagat 82716 

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Gaps

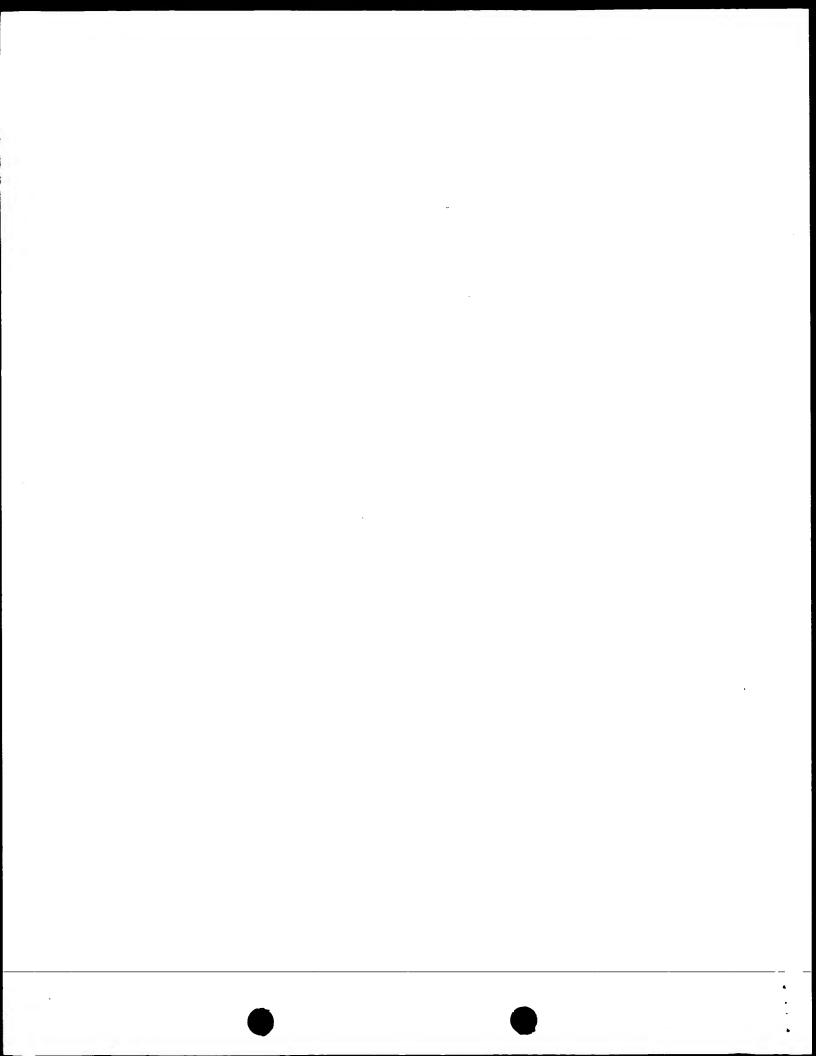
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Length 145750;

Score 23; DB 33; Length 145 Pred. No. 2.50e+00; 0; Mismatches 1; Indels

Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative

Search completed: Tue Dec 2 16:35:46 1997 Job time: 1883 secs.



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Tue Dec 2 17:04:56 1997; Run on:

MasPar time 59.59 Seconds 814.423 Million cell updates/sec ular output not generated

1 ATGAACAAGTTGCTGTGCTG..........AGATAGTTGTGACAGTTTAG 465 TAGTTGTTCAACGACACGAC......TCTATCAACACTGTCAAATC >US-08-915-004-12 (1-465) from US08915004.seq 465 Description: Perfect Score: Sequence

Dbase 0; Query 0 Gap STD Nmatch

TABLE default

Scoring table:

142080 seqs, 52183452 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq28 l:part1 2.part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29

Mean 8.278; Variance 4.498; scale 1.841 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

.76e-28 .76e-28 .87e-28 .87e-28	336- 336- 306- 176- 666-	.48e-1 .30e-1 .61e-1	32e	
Osteoclastogenesis in Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C1 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2	ted OCIF, OCIF ted OCIF, OCIF ted OCIF, OCIF ted OCIF, OCIF	Natriureti Substituted nucleotide nucleotide substituted	ic DNA sequentic DNA sequentic DNA sequentic DNA sequentic DNA sequentic DNA sequentic DNA sequentic DNA sequentic DNA sequentic DNA sequentic DNA sequentic	eneric eneric eneric eneric eneric eneric
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## ALIGNMENTS

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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 22; Page 74; 183pp; Japanese.

This sequence encodes full length osteoclastogenesis inhibitory factor (OCIF) 4. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                    22-APR-1997 (first entry)
Osteoclastogenesis inhibitory factor 4 coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                      Morinaga T;
                                                                                                                                                                                                                                                                                                                     Yasuda H;
                                                                                                                                                                                                                    20-FBE-1996.
20-FBE-1996; JO0374.
20-FBE-1995; JP-05497.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa M, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 G;
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                                                                                                                                 Location/Qualifiers 1..63
                            BP
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LT 1
T36688 standard; DNA; 465 |
T36688;
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                                                                                                       osteoporosis; ss.
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WO9626217-A1.
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                                                                                                                   Homo sapiens
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mat_peptide
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Query Match 100.0%; Score 465; DB 28; Length 465; Best Local Similarity 100.0%; Pred. No. 0.00e+00;

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                                                                                                                                                                                                                                                                                                     gtgtgcgccccttgccctgaccactactacacagacagctggcacaccagtgacgagtgt 240
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                                                                                                                                                                                                                                                                           CTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACC 300
                                                                                                                                                                                                                                                                                                                                                                                      361 CATAGGAGCTGCCTCCTGGATTTGGAGTGGTGCAAGCTGGTACGTGTCAATGTGCAGCA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AFR-1997 (first entry)
Fragment of human OCIF genomic DNA-2.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                            61 CAGGAAACGITITCCICCAAAGIACCIICAITAIGACGAAGAAACCICICAICAGCIGIIG 120
                                                                                                                                        tgtgacaaatgtcctcctggtacctacctaaaaacaacactgtacagcaaagtggaagacc 180
                                                                                                                                                                   121 FGFGACAAAFGFCCFCCFGGFACCFAAAAACAACACFGFACAGCAAAGFGGAAGACC 180
                                                                                                                                                                                                                                                                                                                                                              cataggagotgccotcotggatttggagtggtgcaagotggtacgtgtcaatgtgcagca 420
                                                                                  caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
                           | atgaacaagttgctgtgctgctcgctcgtgttctggacatctccattaagtggaccacc 60
                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding osteoclastogenesis inhibitory factor protein - useful bone resorption control, esp. treatment of osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FdG-1996.
20-FBB-1995; JP-054977.
20-FBB-1995; JP-207568.
21-JdL-1995; JP-207568.
(SNOW) SNOW BRAND MILK PROD CO LTD.
(SNOW) Higashio K, Kobayashi F, Mochizuki S, Morinaga T; Nakagawa N, Shima W, Tsuda E, Ueda M, Yano K, Yasuda H; WPI; 96-402320/40.
                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= g
/note= "encodes residues 252 to 380 of OCIF, see R99925"
WO9626217-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "encodes residues 177 to 251 of OCIF, see R99925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to 112 of OCIF, see R99925'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "encodes residues 113 to 176 of OCIF, see R99925'
                                                                                                                                                                                                                                                                                                                                                                                                                   aaattaattaggatcatgcaaagtcagatagttgtgacagtttag 465
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATTAATTAGGATCATGCAAAGTCAGATAGTTGTGACAGTTTAG 465
 0; Mismatches
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T33183;
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"encodes residues -11
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 465; Conservative
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Claim 91; Page 152-161; 183pp; Japanese.

The sequences given in T33182-83 represent fragment of the genomic DNA encoding the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 50 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419
                                                                                                                                                                                                                                                                                                                                                                                                                              240 tacctacctaaaacaacactgtacagcaaagtggaagacgtgtgcgcccttgccctga 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 ctccttctagtttctggacatctccattaagtggaccacccaggaaacgtttcctccaaa 179
                                                                                                                                                                                                                                                                                                                                                              180 gtaccttcattatgacgaagaaacctctcatcagctgttgtgtgacaaatgtcctcctgg 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 CCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCCGTGTG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 CAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGCGAATG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420 caaggaagggcgctaccttgagatagagttctgcttgaaacataggagctgcctcctgg 479
                                                                                                                                                                                                                                                                                                                              21 CTCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACCCAGGAAACGTTTCCTCCAAA 80
                                                                                                                                                                                                                                                             0; Gaps
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Unman tumour necrosis factor receptor.
Tumour necrosis facor; TNF: receptor; TNF-beta; ligand; tumour;
differentiation; immune response; autoimmune disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                81 GTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccactactacacagacagctggcacaccagtgacgagtgtctatactgcagccccgtgtg
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                                                                                                                                                                                             3187 T;
                                                                                                                                                                                                                        Score 437; DB 27; Length 10190; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                             1899 G;
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                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                             1920 C;
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                                                                                                                                                                                           3184 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC. Fleischmann RD, Greene JM; WPI; 96-433821/43.
                                                                                                                                                                                                                               94.08;
                                                                                                                                                                                                                                           Local Similarity 99.1%;
nes 441; Conservative
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15-MAR-1995; U03216.
15-MAR-1995; WO-U03216.
29-MAR-1995; ZA-002587.
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                                                                                                                                                                                             10190 BP;
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/*tag= a
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New human tumour necrosis factor receptor - used to develop prods.

To treating e.g. tumours, infection, auto:immune disease, graft
rejection, cytocoxicity or inflammation

Claim 1; Fig 1; 59pp: English.

Claim 1; Fig 1; 59pp: English.

Claim 2; Fig 1; 59pp: English.

Claim 3; Fig 1; 59pp: English.

Claim 4; Fig 1; 59pp: English.

Claim 5; Fig 1; 59pp: English.

Claim 6; Fig 1; 59pp: English.

Claim 1; Fig 1; 59pp: English.

Claim 1; Fig 1; 59pp: English.

Claim 1; Fig 1; 59pp: English.

Claim 1; Fig 1; 59pp: English.

The receptor may be used for screening for antagonists and agonists of the receptor and for lighted for the receptor. Such agonists may be used to inhibit the growth of tumours, to stimulate cellular captonist, to required erowine and anti-viral response, to required erowine provide response and anti-viral autofunne diseases, inflammation, septic shock, to inhibit graft.

Control of the receptor and to prevent apoptosis.

Control of the receptor and the provide response and anti-viral autofunne diseases, inflammation, septic shock, to inhibit graft.

Control of the receptor and the provide response and anti-viral autofunne diseases, inflammation, septic shock, to inhibit graft.
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Osteoclastogenesis inhibitory factor 5 coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CAGGAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTG 120
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                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                           DB 28; Length 1173;
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                                                                                                                                                                                                                                                                                                                                               Indels
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F, Mochizuki S,
Ueda M, Yano K,
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21-JUL-1995; JP-207508.
2NOW BRAND MILK PROD CO LTIGOTO W, Higashio K, Kobayashi F, Nakagawa N, Shima N, Tsuda E, Uer PSDB; W99930.
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T36689 standard; DNA; 438 BP.
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20-FEB-1996; J00374.
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claim 24; Page 76; 183pp; Japanese.
This sequence encodes full length osteoclastogenesis inhibitory factor (OCIF) 5. The OCIF of the invention has a molecular weight by SDS-PAGE 06 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treamment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                             121 tgtgacaaatgtcctcctggtacctacctaaaacaacatgtacagcaaagtggaagac 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc 300
                                                                                                                                                                                                                                                                                                                                                                             22-APR-1997 (first entry)
Mutated OCIF, OCIF-CCR4, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                         61 caggaaacgiticciccaaagtacciicattaigacgaagaaaccictcaicagcigiig 120
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                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GIGTGCGCCCCTTGCCCTGACCACTACTACAGACAGCTGGCACACCCAGTGACGAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 cacaaccgcgtgtgcgaatgcaaggaagggcgctaccttgagatagagttctgcttgaaa
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                                                                                                                                                                                                            Score 399; DB 28; Length 438; Pred. No. 1.28e-284;
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                                                                                                                                                                                 94 T;
                                                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                                                 110 G;
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Ueda M, Yano K,
                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                               117 C;
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JF-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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Nakagawa N, Shima N, Tsuda E,
WPI; 96-402320/40.
                                                                                                                                                                               117 A;
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T33176 standard; DNA; 432 BP.
                                                                                                                                                                                                              Match 85.8%;
Local Similarity 99.8%;
les 400; Conservative
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osteo clastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CCR4 in which amino acids 123-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kb under reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. This sequence is not given in the specification and is derived from the protein sequence and the wild type OCIF CDNA sequence given in T36685. Sequence 432 BP; 116 Å; 117 C; 106 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc 300
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Mutated OCIF, OCIF-CBSp, coding sequence. Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; DNA ehcoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 84; Page 149-150; 183pp; Japanese. Morinaga T; Yasuda H; Goto M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40. 20-FEB-1996; JO0374 20-FEB-1995; JP-054977. 21-JUL-1995; JP-207508. (SNOW ) SNOW BRAND MILK PROD CO LTD. Location/Qualifiers T33180 standard; DNA; 564 BP 23-APR-1997 (first entry) 64..561 1..63/product= OCIF-CBsp W09626217-A1. osteoporosis; ss. mat_peptide sig_peptide /*tag= a 29-AUG-1996 Synthetic. 

DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis

Yasuda H; Morinaga

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The protein is adsorbed onto
                                                                                                                          cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
This sequence encodes a mutated version of the full length osteoolastogenesis inhibitory factor (OOIF) of the invention. This sequence encodes OCIF-CBB in which amino acids 167-380 of the mature protein have been deleted. These amino acid changes have been caused by the introduction of a restriction site. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed ont
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Mutated OCIF, OCIF-CDD1, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                                                                                                     in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                         1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                                                                                                                                                                                                                                                                  3; Indels 0; Gaps
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                                                                                                                                                                                                                            124 T;
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20-FEB-1996; JO0374.
20-FEB-1995; JP-05497.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI, 96-40220/40.
                                                                                                                                                                                                                            132 G;
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T33175 standard; DNA; 594 BP.
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Local Similarity 99.3%;
Nes 401; Conservative
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WO9626217-A1.
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Synthetic.
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This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes a mutated version of the invention. This sequence encodes OCIF-CDD1 in which amino acids 177-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 0 KD under reducing conditions and 120 KD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. This sequence is not given in the specification and is derived from the protein sequence and the wild type OCIF CDNA sequence given in T36685. Sequence 594 BP; 176 A; 152 C; 136 G; 130 T;
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Mutated OCIF, OCIF-CDD2, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
                                                                                                                                                                                                                                                                                            Match 85.6%; Score 398; DB 27; Length 594; Local Similarity 99.3%; Pred. No. 7.76e-284; les 401; Conservative 0; Mismatches 3; Indels
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Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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Claim 69; Page -; 183pp; Japanese.
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T33174 standard; DNA; 819 BP
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WO9626217-A1.
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for bone resorption control, esp. treatment of osteoporosis
Claim 66. Page 145; 183p; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DD2 in which amino acids 252.380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 50 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                                                                                                                                                                             Score 398; DB 27; Length 819;
Pred. No. 7.76e-284;
0; Mismatches 3; Indels (
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20-FEB-1996.
20-FEB-1995. JP-054977.
21-JUL-1995; JP-207508.
5NOW DAID MILK PROD CO LTD.
GOCO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
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Best Local Similarity 99.3%;
Matches 401; Conservative
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P-PSDB; R99949
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mat_peptide
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           This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CSph in which amino acids 298-380 of the mature protein have been deleted and replaced by Ser-Leu-Asp. These amino acid changes have been caused by the introduction of a restriction site.

The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kb under reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Mutaqed OCIF, OCIF-DDD1, coding sequence.
Osteqclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
                                                                                                                                                                                                                                                                      Length 966;
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20-FEB-1996; J00374.
20-FEB-1995; JP-205497.
21-UCL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI: 96-402320/40.
                                                                                                                                                                                                                                                                     Score 398; DB 27; I
Pred. No. 7.76e-284;
                                                                                                                                                                                                                                                                                                        0; Mismatches
 81; Page 149; 183pp; Japanese.
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I33170 standard; DNA; 981 BP.
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1 Similarity 99.3%;
401; Conservative
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WO9626217-A1.
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Claim 54, Page 141-142; 185pp, Japanese.

This sequence encodes a mutated version of the full length osteoclassis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DDD1 in which amino acids 178-252 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.

Sequence 981 BP; 312 A; 238 C; 218 G; 213 T;
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CAGGAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTG 120
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Yasuda H;
for bone resorption control, esp. treatment of osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.6%; Score 398; DB 27; Length 981; larity 99.3%; Pred. No. 7.76e-284; Conservative 0; Mismatches 3; Indels (
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a M, Yano K,
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29-AUG-1996;

20-EEB-1996; J00374.

R 20-EEB-1995; JP-054977.

21-JUL-1995; JP-207508.

R 21-JUL-1995; JP-207508.

PA (SNOW ) SNOW BRAND MIK PROD CO LID.

Goto M, Higashio K, Kobayashi F, Mochizuk

Goto M, Shima N, Tsuda E, Ueda M, Yar
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T33171 standard; DNA; 984 BP.
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/product= OCIF-DDD2
WO9626217-A1.
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Matches 401;
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This sequence encodes mutter derivation of the full length of steedlastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes Total mutter actor (OCIF) of the invention. This sequence encodes OCIF-DDD2 in which amino acids 253-356 of the mature protein have been deleted. The OCIF of the invention has a molecular non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                      9t9t9c9ccccttgccctgaccactactacacagacagctggcacaccagtgacgagtgt 240
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T33173;
22-APR-1997 (first entry)
Mutated OCIF, OCIF-CC, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GIGIGGGCCCTIGCCCIGACCACIACIACAGAGAGACAGCIGGCACACCAGIGACGAGIGI 240
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                                                                                                                                                                                                                                                                                                     1 atgaacaacttgctgctgctgcgctcgtgtttctggacatctccattaagtggaccacc 60
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Yasuda H;
                                                                                                                                                                                                                              Score 398; DB 27; Length 984; Pred. No. 7.76e-284; 0; Mismatches 3; Indels
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20-FEB-1995; JP-0374.
20-FEB-1995; JP-207508.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio R, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
 Claim 57; Page 142-143; 183pp; Japanese.
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WO9626217-A1.
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This sequence encodes a mutated version of the full length obsteodlastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CC in which amino acids 331-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Mutated OCIF, OCIF-DCR4, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
                                                                                                                                                                                                                                                                             1 atgaacaacttgctgctgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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Yasuda H;
                                                                                                                                                                                                        Query Match 85.6%; Score 398; DB 27; Length 1056; Best Local Similarity 99.3%; Pred. No. 7.76e-284; Matches 401; Conservative 0; Mismatches 3; Indels 0
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Ueda M, Yano K,
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29-AUG-1996.
20-FEB-1996; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Moc
Nakagawa N, Shima N, Tsuda E, Ueda M,
WPI: 96-402320/40.
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T33169 standard; DNA; 1080 BP.
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osteo clastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CR4 in which amino acids 123-164 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. ocIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption e.g. osteoporosis.
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Osteçclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                                                                                                                          Query Match 85.6%; Score 398; DB 27; Length 1080; Best Local Similarity 99.3%; Pred. No. 7.76e-284;
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207568.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M. Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
P-PSDB; R99948.
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/product= OCIF-CBst
WO9626217-A1.
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mat_peptide
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sequence encodes OCIF-CBst in which Gln371 is substituted with Leu and amino acids 373-380 of the mature protein have been deleted. These amino acid changes have been caused by the introduction of a restriction site. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing on conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the provention of disorders of bone resorption, e.g. osteoporosis.
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Mutated OCIF, OCIF-CL, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis, ss.
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This sequence encodes a mutated version of the full length
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 398; DB 27; Length 1182;
Pred. No. 7.76e-284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yasuda H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 cataggagctgccctcctggatttggagtggtgcaagctggaac 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1996.
20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-19995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Makagawa N, Shima N, Tsuda E, Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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T33172 standard; DNA; 1200 BP
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Local Similarity 99.3%;
hes 401; Conservative
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WO9626217-A1.
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22-APR-1997
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mat_peptide
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Matches
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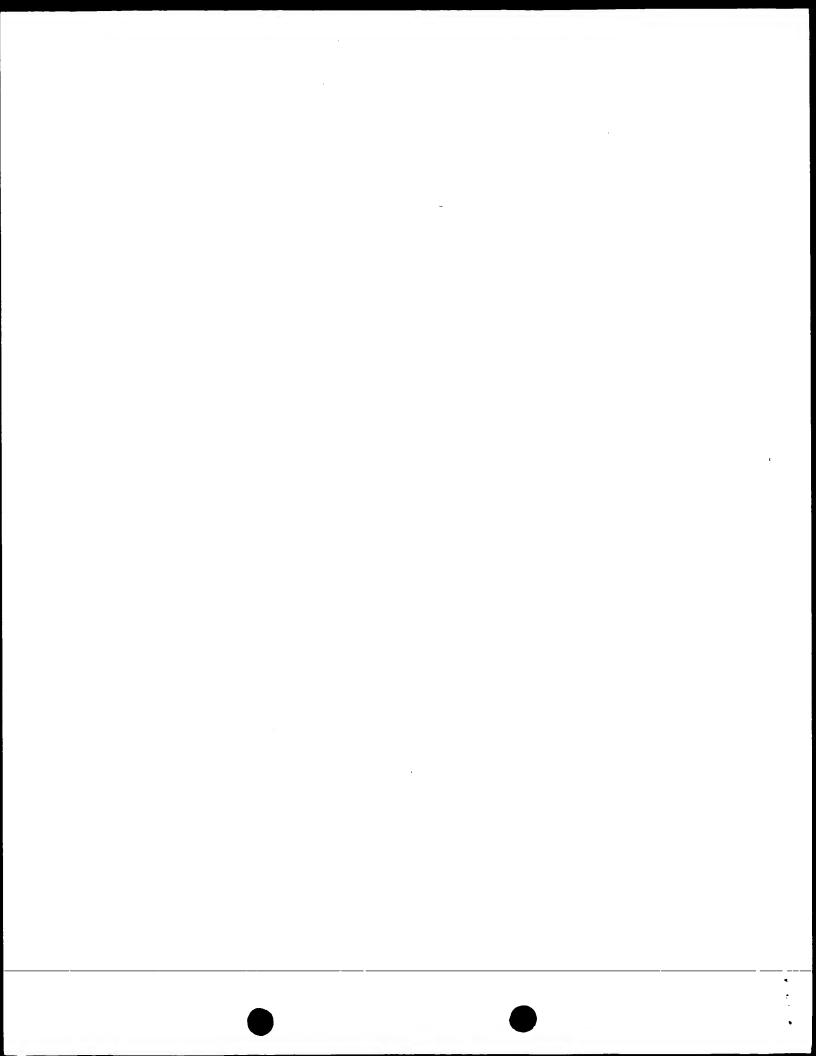
g

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osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CL in which amino acids 379-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
      8888888888888
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ö Gaps ó Query Match 85.6%; Score 398; DB 27; Length 1200; Best Local Similarity 99.3%; Pred. No. 7.76e-284; Matches 401; Conservative 0; Mismatches 3; Indels 0,

- g ò
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      - 241 ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc 300 g ö
- 301 cacaaccgcgtgtgcgaatgcaaggaagggcgctaccttgagatagagttctgcttgaaa 360 g
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- Search completed: Tue Dec 2 17:05:59 1997

Job time : 63 secs.



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

- n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn

MasPar time 292.48 Seconds 816.105 Million cell updates/sec Tue Dec 2 17:06:23 1997; not generated lar output Run on:

>US-08-915-004-12 (1-465) from US08915004.seq 465 ittle: Description: Perfect Score: N.A. Sequence:

1 ATGAACAAGTIGCTGTGCTG..........AGAIAGTIGTGACACTTIAG 465 IACTIGITCAACGACACGAC.......TCIATCAACACTGTCAAAIC

TABLE default Gap 6 Scoring table:

707517 seqs, 256659390 bases x Searched:

Dbase 0; Query 0

Nmatch STD

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

BST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
15:EST1 2:EST2 3:EST3 4:EST1 18:EST13 14:EST14
15:EST15 16:EST10 17:EST11 18:EST18 19:EST13 14:EST14
15:EST15 16:EST22 23:EST23 24:EST38 19:EST39 20:EST30
21:EST31 22:EST22 23:EST23 24:EST38 13:EST31 33:EST33
33:EST33 46:EST40 41:EST41 42:EST42 43:EST43 41:EST43
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57:EST57 58:EST58 59:EST53 66:EST66 67:EST67 68:EST68
69:EST69 76:EST76 77:EST77 78:EST79 79:EST79 74:EST74
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75:EST91 82:EST88 89:EST89 90:EST99 91:EST99 93:EST99
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110:EST118 116:EST118 119:EST118 base:

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7 178:EST178 179:EST179
2 183:EST183 184:EST184
1 188:EST188 189:EST189
2 193:EST193 194:EST194
7 198:EST198
175:EST175 176:EST176 177:EST177 180:EST180 181:EST181 182:EST182 182:EST182 182:EST187 190:EST197 190:EST197 195:EST197 195:EST195 196:EST195 ```

Mean 10.073; Variance 1.752; scale 5.751 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| ( |      | ( ) ( ) X |            |     |            |                                          |          |
|---|------|-----------|------------|-----|------------|------------------------------------------|----------|
| Š | ore  | Match     | Length     | DB  | ΩI         | Description                              | red. No  |
|   | 23   | 4.        | 34.        | 61  | 14106      | rl Homo sapie                            | 72e-07   |
|   | 2 6  |           | ⊃ Ľ        | 171 | 1578       | n4onos.ri stratage<br>x47d01 s1 Homo san | 466-     |
|   | 22   |           | "          | 57  | T42477     | 740 Arabidopsis thal                     | 466-06   |
|   | 22   | •         | 6          | 55  | RICS15559A | ce cDNA, partial s                       | 6e-0     |
|   | 22   | ٠         | Φ          | 117 | 026        | 55c10 Human retina                       | 4.46e-   |
|   | 21   | •         | 0          | 48  | HUM213B09B | uman aorta cDNA 5'-                      | .03e-0   |
|   | 21   | •         | 7          | 13  | . 49       | b42d03.rl Homo sapi                      | .03e-0   |
|   | 21   | •         | 7          | 66  | N61165     | qESTzv27b03.rl Toxo                      | .03e-0   |
|   | 21   |           | 1          | S   | T71088     | c50d04 rl Homo sapi                      | 030-0    |
|   | 21   |           | œ          | 47  | H45707     | p23h05.s1 Homo sapi                      | 036-0    |
|   | 21   |           | σ          | ហ   | T71079     | rl Hom                                   | 036-     |
|   | 21   |           | 4          | Ŋ   | 2155       | ze69b06.sl Soares r                      | 1.03e-0  |
|   | 21   | -         | 4          | œ   | 01102      | e34c01.s1 Soares re                      | .03e-0   |
|   | 21   |           | σ          | 183 | AA098806   | n44d05.sl Stratagen                      | 036      |
|   | 20   |           | -          | 75  | 28E0       | man fetal brain cDN                      | 11e-03   |
|   | 20   |           | C          | 20  | 564        | e06.rl Homo san                          | 11e-0    |
|   | 20   | •         | m          | 55  | RICS11807A | CDNA. partial                            | 116-0    |
|   | 50   | •         | 7          | 7   | 550        | 14c09.rl Homo sap                        | 11e-0    |
|   | 70   |           | ത          | Ó   | HSIMBB115  | sapiens partial                          | 2.11e-0  |
|   | 20   |           | 0          | 140 | 1787       | MGS0003743, Huma                         | .11e-    |
|   | 20   | ٠         | 2          | Ŋ   | T71171     | 52c03.rl Homo sap                        | e-03     |
|   | 70   |           | 4          | N.  | T72764     | c51a10.rl Homo sap                       | .11e-0   |
|   | 0 0  |           | စေး        |     | H83210     | 103.rl Homo sa                           | .11e-03  |
|   | 9 0  | ٠         | <u> </u>   | 1/3 | W/263/     | JeU7.sl Soares                           | 2.11e-   |
|   | 7 (  | ٠         | <b>~</b> r | χο. | K98014     | r02.sl Homo sap                          | le-03    |
|   | 7 0  | •         | <b>∽</b> t | 140 | 7.74       | STUG SCRISTOS                            | . Tie    |
|   | ) (C | •         | <b>~</b> I | ~ ( | AA067387   | 32 Lambda-PRL2 A                         | 2.11e-0  |
|   | 07   | •         | /          | 2   | 303        | f02.rl Homo sapi                         | 11e - 03 |
|   | 70   | -         | _          | 178 | AA072548   | SLD058T3 Brugia                          | 11e-     |
|   | 50   | •         | g          | 7   | W79653     | 3h08.rl Soar                             | .11e-0   |
|   | 20   |           | _          | ^   | W79538     | lg01.s1 Soares f                         | 2.11e-0  |
|   | 20   |           | ч          | 7   | 207        | a06.sl Homo sapi                         | 11e-03   |
|   | 20   | •         | Н          | 185 | AA135635   | 1dl0.sl Soares                           | .11e-0   |
|   | 70   | ٠         | П          | ā   | W51540     | SLC915T3 Bruqia m                        | .11e-0   |
|   | 20   | •         | C          | σ   | H94319     | 3b09.s1 Soares fe                        | 11e-     |
|   | 20   |           | N          | 53  | R92022     | e05.sl Homo sapie                        | .11e-03  |
|   | 20   | •         | 2          | 75  | H97994     | J6e04 sl Homo sapi                       | 11e-0    |
|   | 70   |           | m          | 89  | H72171     | 99906 rl Homo s                          | 116-0    |
|   | 20   |           | 4          | Ö   | C20472     | ice cDNA, partial s                      | 2.11e-0  |
|   | 70   |           | 4          | 165 | C20089     | ice cDNA, partial s                      | .11e-0   |
|   | 20   |           | S          | Õ   | N74503     | 4h03.sl Homo sap                         | 11e-     |
|   | 20   |           | S          | 74  | н93069     | J6h02.sl Homo sapie                      | 11e-03   |
|   | 20   |           | 9          | 193 | AA166259   | 9dll.rl Life                             | 2.11e-   |
|   | 0    |           |            |     |            |                                          | ֡        |

## ALIGNMENTS

|          | EST 10-JUL-1995 | ym62a05.rl Homo sapiens cDNA clone 163472 5' similar to SP:S32367 |                |           |         |          |
|----------|-----------------|-------------------------------------------------------------------|----------------|-----------|---------|----------|
|          | _               | clone                                                             |                |           |         |          |
|          | mRNA            | CDNA                                                              | Z              |           |         |          |
|          | 344 bp          | 1 Homo sapiens                                                    | PA-SNAP PROTEI |           |         |          |
|          | H14106          | ym62a05.rl                                                        | S32367 AL      | H14106    | g878954 | EST.     |
| RESULT 1 | LOCUS           | DEFINITION                                                        | •              | ACCESSION | NID     | KEYWORDS |

SOURCE

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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 4.7%;
Local Similarity 71.2%;
hes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 C
                                                                                                                              Contact: Wilson RK
                                                                            Unpublished (1995)
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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                                                                                                 COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                             double-stranded conva was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT/T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured a ortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopteraydi; Choanata; Tetrapoda; Anniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 344)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z146h08.rl Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 550527 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                     vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampidillin resistant) primer=M13RP1 Rsitel=Not I Rsite2=Eco RI 55-year old male. 1st strand cDNA was primed with a Not I oligo(dT) primer [6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stops: 313 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 300)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
human clone=163472 library=Soares adult brain N2b4HB55Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 gcaccacttcccctnactactnctacncacacagct 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 GCGCCCCTTGCCCTGACCACTACTACACAGACAGCT 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                              midbrain, pons and medulla.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
WashU-Merck EST Project
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116 c
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Best Local Similarity 77.8%;
Matches 28; Conservative
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human clone-264865 primer=m13 -40 forward library-Soares melanocyte
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                            Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-1995
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1 (bases 1 to 453)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. WashU-Merck EST Project
                                                                                                                                                                                                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N21157 453 bp mRNA EST 19-DEC yx47d01.s1 Homo sapiens cDNA clone 264865 3' similar to SP:TCPB_MOUSE P80314 T-COMPLEX PROTEIN 1, BETA SUBUNIT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 gtaacttcattgcaaccacgaaacctgtaatacgctgtacagtaacaagtgt 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Stratagene HeLa cell s3 937216" /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22; DB 183; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 others
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                                                                                                                                                         WashU-Merck EST Project
Washington University School of Medicine
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Gaps

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\bar{\rm EST}({\rm expressed}\ {\rm sequence}\ {\rm tag}) . Organ shoot (8 days old) cDNA to Oryza sativa (strain Nipponbare, ) Green shoot (8 days old) cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W29026 796 bp mRNA EST 08-MAY-1996
55clO Human retina cDNA randomly primed sublibrary Homo sapiens
                                                                                                                                                                                                                                         27-JUL-1995
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Macke, J., Smallwood, P. and Nathans, J. Adult Human Retina cDNA Oupublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Dr. Jeremy Nathans
Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 cgggtgcantnacggcaaccaggtgctcaaggagctngaggaggccaagaaggngt 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 cGAGTGTCTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGT 289
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnollophyta;
Liliopsida; Poales; Poaceae; Oryza.
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                                                                                                                                  64 GAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAG 114
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                      Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 others
                                                              0; Mismatches 16; Indels
                                                                                                           365 gaaacagttgctgnaagctaccttgagtttgcccaagaaacccttnatnag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Nipponbare"
/dev_stage="Green shoot (8 days old)"
147 c 150 g 93 t 5 ot)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice Genome Research Program
National Institute of Agrobiological Resources
                      Score 22; DB 57; ; Pred. No. 4.46e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22; DB 55;
Pred. No. 4.46e-06;
                                                                                                                                                                                                                     RICS15559A 493 bp mRNA Rice cDNA, partial sequence (S15559_1A). D48963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki,T., Miyao,A. and Yamamoto,K.
Rice cDNA from shoot
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-Feb-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Best Local Similarity 66.1%;
Matches 37; Conservative
                    Query Match
Best Local Similarity 68.6%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phone: 0298-38-7441
Fax : 0298-38-7468
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                                                                                                                                                                                                                                                                                                                                                                    mRNA.
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ACCESSION
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SOURCE
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                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thale cress clone=113K15T7 library=Lambda-PRL2 strain-var columbia vector=lambda 2ip-Lox primer=T7 dye primer Rsitel=Sal Rsite2=Not Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated eticlated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 472)
Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H.,
McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;
Brassicaceae; Arabidopsis.
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                                                                                                                                                                                          High quality sequence stops: 321
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-1995
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Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                            WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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T42477
gg33235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 111;
Pred. No. 4.46e-06;
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                                                                                                                                                                        Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dery Match
Best Local Similarity 77.5%;
Matches 31; Conservative
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                                            Contact: Wilson RK
  Unpublished (1995)
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Fax: 517-353-9168
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Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 325)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Washly-Merck Est Project

Washly-Merck Est Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read.
                                                                                                                                                                                                                                              08-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-1996
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TGESTZY27b03.r1 Toxoplasma gondii cDNA clone tgzy27b03.r1 5'
similar to SW:EFIA_PLAFK Q00080 ELONGATION FACTOR 1-ALPHA ;.
N61165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                 2047904 325 bp mRNA EST 08-FE yb42d03.r1 Homo sapiens cDNA clone 73829 5' similar to 95:03910_rnal Human (HUMAN).
T54964
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                                                                                                  131 aahthtotbagaatccatcttaataaataahttaahhhcacaataaaacgt 181
                                                                                                                      Length 300;
       Score 21; DB 48; Length 300;
Pred. No. 1.03e-04;
6; Mismatches 15; Indels
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    Query Match
4.5%;
Best Local Similarity 58.8%;
Matches 30; Conservative
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                                                                                                                                                                                                                                /organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
Site_2: EcoRI; The library used for sequencing was a sublibrary derived from a human retina cDNA library.
Inserts from retina cDNA library DNA were isolated,
Inserts from retina cDNA library DNA were isolated,
Inserts from retina cDNA library DNA were isolated,
Into lambda gtl0. Individual plaques were arrayed and
used as templates for PCR amplification, and these PCR
products were used for sequencing."
/clone_lib="Human retina cDNA randomly primed sublibrary"
/sex="mixed (males and females)"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="E. coli strain K802"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 300).
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takalchi, A., Takada, S., Matanabe, T., Takahashi, E. T., Hirai, Y., Unpublished(003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (library: Clontech human aorta polyA+ mRNA (#6572)) cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST(expressed sequence tag); Human aorta; similar to known(May 29,1995).
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/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
49 c 32 g 85 t 14 others
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4.7%; Score 22; DB 117; Length 796;
Best Local Similarity 73.9%; Pred. No. 4.46e-06;
Matches 34; Conservative 0; Mismatches 12; Indels (
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                                            Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
                                                                                                                                       BACKWARD: GAGGTGGCTTATGAGTATTTCTTCCAGGGTAA
Seg primer: GGGTAAAAAGCAAAAGAATT.
Location/Qualifiers
                                                                                           PCR PRIMERS
FORWARD: CITITGAGCAAGITCAGCCTGGITAAGT
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Submitted (30-May-1995) to DDBJ by:
Tsutomu Fujiwara
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Human aorta cDNA 5'-end GEN-213B09.
D56616
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Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho
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Tel: 410 955 4678
Fax: 410 614 0827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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31-JUL-1995

Gaps

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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Anniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 383)
Hiller, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Hultman, M., Rubada, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Treyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fmail: estewatson.wustl.edu
High quality sequence stops: 268
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                              Score 21; DB 5; Length 376;
Pred. No. 1.03e-04;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                              ' 383 bp mRNA EST
yp23h05.s1 Homo saplens cDNA clone 188313 3'.
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                                                                                                                                                                                                                                 DB 47;
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                                        /organism="Homo sapiens"
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Location/Qualifiers
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79 c 9
                                                            /clone="84103"
105 c
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Matches 27; Conservative
                                                                                                                                   Ouery Match
Best Local Similarity 78.4%;
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                             Source: David Sibley, Washington University Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human clone=84103 library=Stratagene liver (#937224)
vector=pBluescript SK host=SOLR cells (kanamycin resistant)
primer=M13RP1 Rsitel=ECORI Rsite2=xhoI cloned unidirectionally.
Primer: Oligo dT. Hepatectomy from normal 49 year old male
caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; 5
adaptor sequence: 5'-GAATTCGGCACGAG-3'; 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 372)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
Unpublished (1995)
                                                                                                  Ajioka,J.A., Aslett,M.A., Dietrich,N., Dubuque,T., Kucaba,T.,
Marta,M., Sibley,L.D., Wan,K.L. and Waterston,R.A.
Washb-Merck Toxoplasma EST Project
Unpublished (1996)
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                 Eukaryotae, mitochondrial eukaryotes; eukaryote crown group;
Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystida;
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Washureck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                              WashU-Merck EST Project
Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Toxoplasma gondii"
/clone="tgzy27b03.r1"
/strain="RH"
                                                                                                                                                                                                                                                                                                                                            Email: toxo@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Best Local Similarity 73.3%;
                                                            Toxoplasma.
1 (bases 1 to 371)
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -4.0M13 from Amersham
High quality sequence stop: 417.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Insert Length: 603 Std Error: 0.00
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Socres,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/lab_bost="HH10B (ampicillin resistant)"
complement(<1...447)
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/sex="male"
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WashU-Merck EST Project
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ze69b06.s1 Soares retina N2b4HR Homo sapiens cDNA clone 364211 3'.
AA021559
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                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers
                                          01-MAR-1995
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trenskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
yc50c04.rl Homo sapiens cDNA clone 84102 5' similar to gb:J03910_rnal Human (HUMAN);.
                                                                                                                                                                                                                                        human clone=84102 library=Stratagene liver (#937224)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 395;
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0; Mismatches 8
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/clone="84102"
a 105 c 91 g 110
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Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project Unpublished (1995)
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WashU-Merck EST Project
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Best Local Similarity 78.4%;
Matches 29; Conservative
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BASE COUNT

ORIGIN

FEATURES

DEFINITION

RESULT

ACCESSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE JOURNAL

COMMENT

0; Gaps

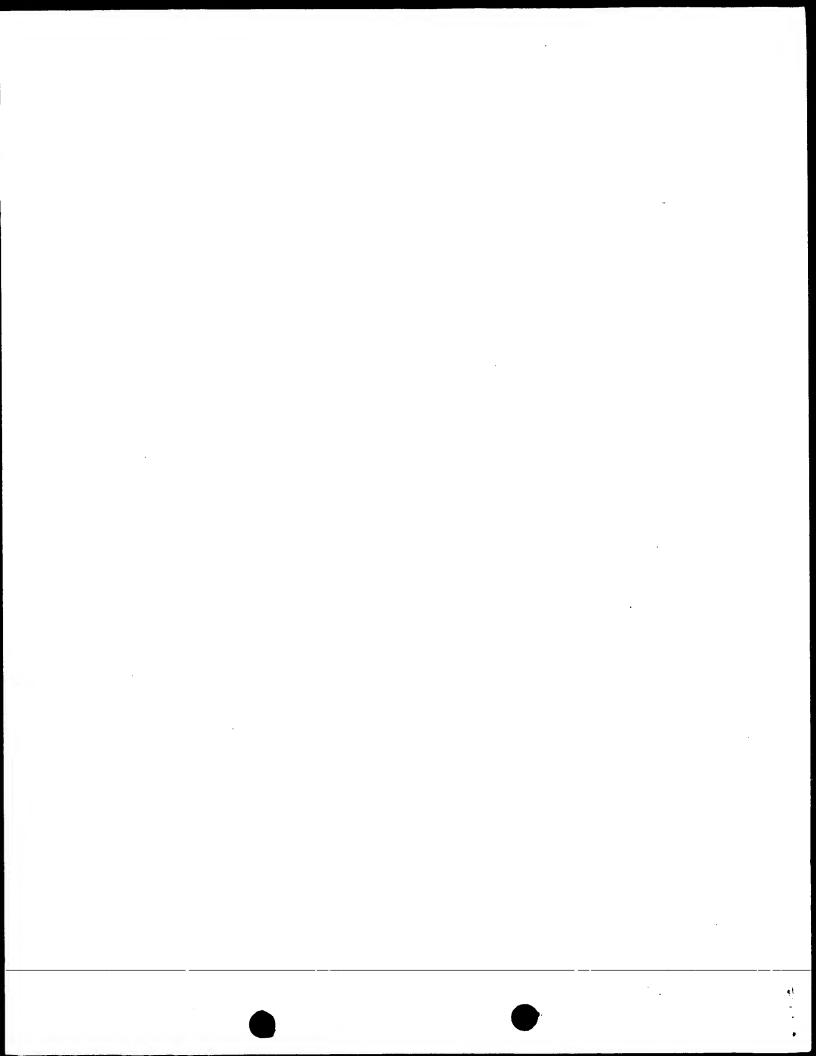
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20-C111930
20144065.s1 Strategene HeLa cell s3 937216 Homo sapiens CDNA clone 550281 3' similar to SW:NIZM_BOVIN Q02369 NADH-UBIQUINONE AAA098806
91644777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4644 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 423.
Location/Qualifiers
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotze; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 491)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Wasterston, R., Williamson, A., Wohldmann, P.; and Wilson, R. Unpublished (1995)
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Pred. No. 1.03e-04;
0; Mismatches 6; Indels
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                 High quality sequence stop: 415.
Location/Qualifiers
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Seq primer: mob.REGA+ET
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WashU-Merck EST Project
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Local Similarity 81.8%;
les 27; Conservative
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AUTHORS
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JOURNAL
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                                 FEATURES
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Xhol; Cloned unidirectionally. Primer: Oligo dT. HeLa
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                                                                           /clone_lib="Stratagene HeLa cell s3 937216"
/sex="female"
                                                                                                                                                                                       Score 21; DB 183; Length 491;
Pred. No. 1.03e-04;
0; Mismatches 5; Indels C
                                                                                                                                                                                              .03e-04;
-heq 5; Indels
                                                                                                      /dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
complement(<1..>491)
                                                                                                                                               104 t
                                                                                                                                             134 g
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Best Local Similarity 83.9%;
Matches 26; Conservative
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Search completed: Tue Dec 2 17:11:26 1997 Job time : 303 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

 n.a. database search, using Smith-Waterman algorithm n.a. MPsrch\_nn MasPar time 152.68 Seconds 836.954 Million cell updates/sec Tue Dec 2 17:11:48 1997; Run on:

not generated ular output ritle:

>US-08-915-004-12 (1-465) from US08915004.seq 465 Description: Perfect Score: N.A. Sequence:

......AGATAGTTGTGACAGTTTAG 465 1 ATGAACAAGTIGCTGTGCTG TACTTGTTCAACGACACGAC

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch

359085 seqs, 137405154 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1.EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204 7:EST205 8:EST206 9:EST207 10:EST208 11:EST209 12:EST210 13:EST211 14:EST212 15:EST213 16:EST213 17:EST213 15:EST213 15:EST223 15:EST223 15:EST223 15:EST223 15:EST223 15:EST223 15:EST223 15:EST223 15:EST223 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23 15:EST23

tabase:

Mean 10.125; Variance 1.771; scale 5.717 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1.32e-07 3.31e-06 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 1.47e-03 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AA203500 874 bp mRNA EST 24-JAN-1997 2x58h07.rl Soares fetal liver spleen INFLS S1 Homo sapiens CDNA clone 446749 5' similar to contains element MSR1 repetitive element Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 874)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and Homo sapiens AA203500 91799268 Wilson, R. human. RESULT 1 LOCUS DEFINITION SOURCE ORGANISM ACCESSION REFERENCE AUTHORS NID KEYWORDS

Contact: Wilson RK

The WashU-Merck EST Project

Unpublished (1995)

TITLE JOURNAL COMMENT

Query Result

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standard; DNA; STS; 204 BP
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                                                                                                                                                                                                                                                                                                                                 human .
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BASE COUNT
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                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28N13 rev2 from Amersham
High quality sequence stop: 307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newman T., deBruijn F.J., Green P., Keegstra K., Kende H., McIntosh L., Ohlrogge J., Raikhel N., Somerville S., Thomashow M., Retzel E., Somerville C.; Referes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGIS; 142477; AGIS July 1995.

Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bidg., E. Lansing, Mi Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn6tbm.cl.msu.edu. NCBI gi: 933235

Key
          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Bukaryotae, mitcohondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (ampicillin resistant)"
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WashU-Merck EST Project
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12-MAR-1997 (Rel. 51, Last upda
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Local Similarity 72.5%;
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MEDLINE; 95148729.
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2q16e09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 629896 3' similar to SW:MAPB_HUMAN P46821 MICROTUBULE-ASSOCIATED PROTEIN 1B. ;.
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Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@mage.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Possible reversed clone: poly1 not found
Seq primer: -41ml3 fwd. Er from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 431)
Hillar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
Washerston, K., Milliamson, A., Wohldmann, P., and Wilson, R.
Unpublished (1995)
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                 Sequence 472 BP; 126 A; 97 C; 100 G; 137 T; 12 other;
                                                                                                                                           Score 22; DB 77; Pred. No. 3.31e-06;
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                        /strain="var columbia"/note="thale cress"
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/clone="113K15T7"
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                                                                                                                                           // Match
Local Similarity 68.6%;
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Best Local Similarity 71.7%;
Matches 33; Conservative
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Gaps

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Homo sapiens (tissue library: LANL flow sorted chromosome 5 library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/tissue_lib="LANL flow sorted chromosome 5 library in
M13mp18"
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 204)
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                                    Score 20; DB 46; Length 204
Pred. No. 1.47e-03;
0; Mismatches 12; Indels
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Best Local Similarity 72.7%; Pred. No. 1.47e-03;
Matches 32; Conservative 0; Mismatches 12; Indels
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                                                                                                                     127 TGTCACACAACAGCTGATGAGGTTTCTTCGTCATAATGAAGG 84
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/evidence=experimental
/note="for primer B"
/7 c 38 g
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                                                                                                                                                                                     HUMBER CHROMOSOME 5 LANL STS 200.
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/evidence=experimental
/note="for primer A"
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Human chromosome 5 LANL STS 200
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Genomics 32 (1), 91-96 (1996)
96230329
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Location/Qualifiers
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                                    Query Match
Best Local Similarity 72.7%;
Matches 32; Conservative
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M13mp18"
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/tissue_llb="LANL flow sorted chromosome 5 library in
M13mp18"
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Grady, D.L.
                                                                                                                                                                         Grady D.L., Robinson D.L., Gersh M., Nickerson E., McPherson J., Wasmuth J.J., Overhauser J., Deaven L.L., Moyzis R.K.; "The generation and regional localization of 303 new chromosome sequence-tagged sites"; Genomics 32:91-96(1996).
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                                                                                          Homo sapiens (human)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Frimates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="for primer B" Sequence 204 BP; 53 A; 47 C; 38 G; 66 T; 0 other;
                            24-JAN-1996 (Rel. 46, Created)
18-MAR-1997 (Rel. 51, Last updated, Version 3)
Human chromosome 5 LANL STS 200.
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complement(2..26)
/evidence=experimental
/note="for primer A"
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/note="5qp"
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L28249
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/evidence=EXPERIMENTAL
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/evidence=EXPERIMENTAL
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/note="for primer B"
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Location/Qualifiers
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/tissue_lib="LANL flow sorted chromosome 5 library in
M13mp18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/brugia/L2S/MBL2SJ8A6T3.html Seg primer: T3.
Location/Qualifiers
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Secerpentea; Spiruria; Spirurida; Filarioidea; Onchocercidae;
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09-MAR-1997 (Rel. 51, Last updated, Version 1)
MBL2SJØR6T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJØR6
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61 A; 47 C; 56 G; 70 T; 1 other;
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172..197
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/note="for primer B"
/note="for gramer B"
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/evidence=experimental
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                                                       /chromosome="5"
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/octe="vector: lambdaZapII; Site_1: Eco R I (5' end); Site_2: Xho I (3' end); Brugia malayi is a lymphatic filarial nematode parasite of humans. Full length cDNA was prepared by long-range RT-PCR from mRNA from L2 larvae of the human filarial nematode parasite Brugia malayi using nematode spliced leader (SL, 5'end) and oligo-d(T) (3' end) primers. The library had an unamplified titre of -1 x 10E6 per ml and -95% of clones have inserts (mean length -900 bp). The library is available from The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, MA 01063 USA phone +1 413 585 3826 fax +1 413 585 3786 email
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University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
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Blaxter, M.L., Waterfall, M., Daub, J., Lizotte, M., Baron, L. and
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MBL28J8A6F3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJ8A6 5'
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/sex="mixed"
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/strain="TRS Labs"
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Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
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Best Local Similarity 81.3%;
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/dev_stage="mosquito derived, second stage larvae (L2)"
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Blaxter,M.L., Waterfall,M., Daub,J., Lizotte,M., Baron,L. and
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Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae;
                                                                                                                                                                                                                                                                      Contact: Blaxter ML Institute of Cell, Animal and Population Balology University of Edinburgh Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JT, UK. Tell: +44 131 650 6760 Fax: +44 131 670 540 Email: mark.Dlaxter@ed.ac.uk The ABI trace of this
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MBL2850H3T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJ0H3 5'
g1870877
                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/brugia/L2S/MBL2SJ0H3T3.html Seq primer: T3.
Location/Qualifiers
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Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae;
                       AA241559;
91870877
09-MAR-1997 (Rel. 51, Created)
09-MAR-1997 (Rel. 51, Last updated, Version 1)
MBL2SJOH3T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJOH3
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Sequence 308 BP; 93 A; 65 C; 70 G; 80 T; 0 other;
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/strain="TRS Labs"
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            standard; RNA; EST; 308 BP
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Local Similarity 81.3%;
les 26; Conservative
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            BMAA41559
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/note-"vector: lambdazapII; Site_1: Eco R I (5' end); Site_2: Xho I (3' end); Brugia malayi is a lymphatic filarial nematode parasite of humans. Full length colls was prepared by long-range RT-PCR from mRNA from L2 larvae of the human filarial nematode parasite Brugia malayi using nematode spliced leader (5L, 5' end) and oligo-d(T) (3' end) primers. The library had an unamplified titre of 1 x 10E6 per ml and -95% of clones have inserts (mean length -900 bp). The library is available from The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center: Smith College, Northampton, MA 01063 USA phone +1 413 585 3826 fax +1 413 585 3786 email
                                                                                                                                       Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
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/lab_host="E. coli XL1-Blue MRF-"
<1..>308
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Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan
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                                                                                                                                                                                                                                                                                                Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
The Ail trace of this sequence can be viewed at
http://www.sanger.ac.uk/brugia/L2S/MBL2SJOH3T3.html
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Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
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1.47e-03;
..hoq 6; Indels
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28-SEP-1996 (Rel. 49, Created)
12-MAR-1997 (Rel. 51, Last updated, Version 5)
26232 Lambda-PRL2 Arabidopsis thaliana cDNA clone 88F5T7
Genes expressed in adult female Brugia malayi
Unpublished (1996)
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Pred. No. 1.47e-
0; Mismatches
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/strain="TRS Labs"
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/clone_lib="JHU96SL-BmL2"
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                                                                                                                                                                                                                                                                         Tel: +44 131 650 6760
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Best Local Similarity 81.3%;
Matches 26; Conservative
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/organism="Arabidopsis thaliana"
/strain="var columbia"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal quantitie
                                                                                                                                                                                                                                              on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The CDNA inserts were directionally cloned with Sal-Notarms using oligo dT prime
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State University MSU-DOE-PRL, Michigan State University, Plant Biology Blog. E. Lansing.MI Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@ibm.cl.msu.edu Seq primer: T7. Exemple Desation.cl.msu.edu Seq primer: T7.
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Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae;
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09-MAR-1997 (Rel. 51, Last updated, Version 1)
MBL2SJ9D7T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJ9D7 5′
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/clone_lib="Lambda-PRL2"
Sequence 377 BP; 100 A; 93 C; 64 G; 105 T; 15 other;
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larity 73.2%;
Conservative
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/note="Vector: lambdaZapII; Site_1: Eco R I (5' end):
Site_2: Xho I (3' end); Brugia malayi is a lymphatic
filatial nematode parasite of humans. Full length cDNR was
prepared by long-range RT-PCR from mRNA from L2 larvae of
the human filatial nematode parasite Brugia malayi using
nematode spliced leader (SL, 5'end) and oligo-d(IT) (3'
end) primers. The library had an unamplified titre of -1 x
10E6 per ml and -95% of clones have inserts (mean length
-900 bp). The library is available from The Filarial
Genome Project Resource Center: contact Dr. S.A. Williams,
Clark Science Center, Smith College, Northampton, MA 01063
USA phone +1 413 SBS 3826 fax +1 413 SBS 3786 email
primers. The library had an unamplified titre of ~1 x 10E6 pper ml and ~95% of clones have inserts (mean length ~900 bp). The library is available from The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, MA 01063 USA genome@smith.smith.edu."
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/lab_host="E. coli XL1-Blue MRF-"
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The AbI trace of this sequence can be viewed at
http://www.senger.ac.uk/Doruglak/Li2S/MBL2SJ9D7T3.html This is the
full sequence of the cDNA clone. The polyA tail has been clipped
and is excluded from this sequence
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MBL28J9D7T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJ9D7 5'.
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Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae;
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Pred. No. 1.47e-03;
0; Mismatches 6
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/strain="TRS Labs"
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/sex="mixed"
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Fax: +44 131 670 5450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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/clone\_lib="JHU96SL-BmL2"

1

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forganism="Brugia malayi"

forganism="TRS Labs"

fore-"Vector: lambdaspII: Site_1: Eco R I (5' end);

site_2: Xho I (3' end); Brugia malayi is a lymphatic

filarial nematode parasite of humans. Full length cDNA was

prepared by long-range RT-PCR from mRNA from L2 larvae of

the human filarial nematode parasite Brugia malayi using

nematode spliced leader (SL, 5'end) and oligo-d(I) (3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primers. The library had an unamplified titre of -1 x 10E6 per ml and -95% of clones have inserts (mean length -900 bp). The library is availablefrom The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, Ma 01063 USA genome@smith. SMS 3826 fax +1 413 585 3786 email
                                                                                                                                                                                                                      ;
0
/sex="mixed"
/dev_stage="mosquito derived, second stage larvae (L2)"
/lab_host="E. coli XL1-Blue MRF-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="mosquito derived, second stage larvae (L2)"
/lab_host="E. coli XLI-Blue MRF-"
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Blaxter ML Institute of Cell, Animal and Population Biology University of Edinburgh Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JT, UK. Tel: +44 131 650 6760 Fax: +44 131 670 5450 Email: mark.blaxter@ed.ac.uk The ABI trace of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence can be viewed at http://www.sanger.ac.uk/brugia/L2S/MBL2SJ0B3T3.html This is the full sequence of the cDNA clone. The polyA tail has been clipped and is excluded from this sequence Seq primer: T3.

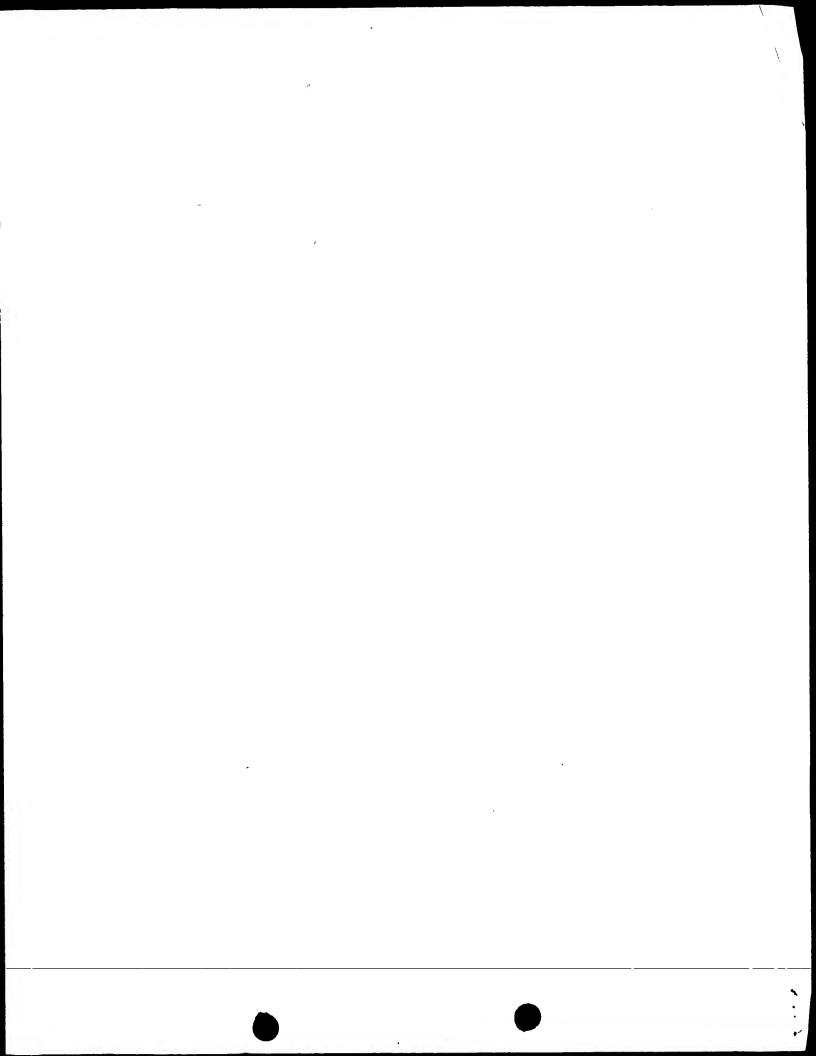
Key
                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae;
                                                                                                                                                                                                                                                                                                                                                                                                                        09-WAR-1997 (Rel. 51, Created)
09-MAR-1997 (Rel. 51, Last updated, Version 1)
MBL2SJ0E3T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJ0E3 5'.
                                                                                                                                                                      Score 20; DB 67; Length 383;
Pred. No. 1.47e-03;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.3%; Score 20; DB 79; Length 387;
Best Local Similarity 81.3%; Pred. No. 1.47e-03;
Matches 26; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blaxter M.L., Waterfall M., Daub J., Lizotte M., Baron L.,
                                                                                                                       2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <1..>387
BP; 121 A: 65 C; 78 G; 123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Genes expressed in adult female Brugia malayi";
                                                                                                                     120 t
                                                                                                                                                                                                                                                  136 gtacgtatcaatggtcagcaaagcaatcagg 167
                                                                                                                                                                                                                                                                         401 GTACGTGTCAATGTGCAGCAAATTAATTAGG 432
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                                                                                                                                                                                                                                                                                                                                                                      BMAA41525 standard; RNA; EST; 387 BP
                                                                                                                 78 g
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                                                                                                                                                                          Query Match
Best Local Similarity 81.3%;
Matches 26; Conservative
                                                                                                                   67 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones S.J.;
                                                                                                                                                                                                                                                                                                                                                                                    AA241525;
91870843
                                                                                                               BASE COUNT
ORIGIN
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Gaps

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401 GTACGTGTCAATGTGCAGCAAAATTAATTAGG 432
137 gtacgtatcaatggtcagcaaagcaatcagg 168
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Search completed: Tue Dec 2 17:14:28 1997 Job time: 160 secs.



| MPSICh_nn n.a Run on: TILLE: Description: Perfect Score: N.A. Sequence: Comp: Scoring table: Scoring table: Bearched: Searched: Database: Batabase:                                                                                                                                                                               |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Database:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | STR 94:SYN 95:UNA 96:VRL1 97:VRL2 98:<br>0:VRL5 101:VRL6 102:VRL7 103:VRL8 104:                                                                                                 |
| Database:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV<br>112:MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRI2<br>118:ROD 119:SYN 120:UNA 121:VRL<br>u-embJS0_99<br>122:part1         |
| Statistics:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Mean 10.182; Variance 3.871; scale 2.630                                                                                                                                        |
| Pred. No.<br>score gree<br>and is der                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. |

SUMMARIES

| ed. R       | 7.95e-03<br>2.36e-03<br>6.05e-03<br>1.31e+00<br>1.31e+00<br>1.31e+00<br>1.31e+00<br>1.31e+00<br>1.31e+00<br>1.31e+00<br>1.31e+00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | .68e+0                                                                 | .68e+0<br>.68e+0                                                                                | .68e+0<br>.33e+0<br>.33e+0<br>.33e+0                                                             |                                                                                                                                           | 2.33e+0<br>2.33e+0<br>2.33e+0               | 2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.3)e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2.33e+(2. | 2.33e+<br>2.33e+(<br>2.33e+(                          | 2.33e+(<br>2.33e+(<br>2.33e-<br>n<br>2.33e- | -ocr-1996                                                              | ir use to                                                                                                          |                                  |
|-------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------|---------------------------------------------|------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------|----------------------------------|
| Description | Sequence 5 from paten 2. Sequence 5 from paten 2. R. norvegicus mRNA for 6. C. reinhardtii phospho 0. cuniculus Sp17 gene 1. M. musculus tumor necr 1. Mouse tumor necrosis 2. Murine tumor necrosis 1. Murine tumor necrosis 1. Murine tumor necrosis 1. Murine tumor necrosis 1. Murine tumor necrosis 1. Murine tumor necrosis 1. Murine tumor necrosis 1. E. amylovara (Ea7/74) 1. C. Anylovara (Ea7/74) 1. C. Anylovara (Ea7/74) 1. C. Alamydomonas reinhar 5.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Maize glucathione S-t<br>Porcine DNA for musca<br>S.purpuratus nuclear | BOS taurus muscarinic<br>M.leprae genes rplL,<br>Human herpesvirus-7 (<br>Human DNA sequence ** | Human DNA sequence **<br>Sequence 2 from paten<br>Sequence 13 from pate<br>H.sapiens H2B/h gene. | Homo sapiens GT212 mR 2 D.melanogaster annexi 2 B.pendula mRNA encodi B.pendula mRNA encodi Glycine max glycxysom 2 m acetivum ribulose-1 | Trichoderma harzianum D.melanogaster anxx g | Drosophila melanogast<br>Azotobacter chroococc<br>Bacteroides thetaiota<br>Mouse mRNA for PC6B,<br>D.subobscura DNA homo                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ytomegalovirus<br>thabditis elegan<br>pro-alphal type | 200                                         | 30. PAT 30                                                             | A. and Stotz,H.<br>acturonases and the                                                                             | 26 t 141 others                  |
| ΙD          | 128278<br>128278<br>128278<br>128278<br>CREPHOSF1<br>MCTHERA<br>MMTHERA<br>MMTHERA<br>MMTHERA<br>MMTHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHERA<br>MMATHE | MZEGSTIA.<br>SSACHRM<br>SPASSUBA                                       | MLB1790G<br>HHU43400<br>HS435D1                                                                 | HS435D1<br>I15665<br>I14734<br>HSH2BH                                                            | HUMGT212A<br>DROANNX<br>BPPT<br>BPPT<br>SOYICLIA                                                                                          | THU05192<br>DMANX<br>DMANX                  | DRO14DC2Z<br>ACVNFDGK<br>BNRRTEAB<br>MUSPC6B<br>DSPTEH1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                       |                                             | ALIGNMENTS<br>p DNA<br>ent US 55698                                    | ch,J.M., Por<br>fungal pola<br>ase<br>A 5 29-OCT-                                                                  | Qualifiers<br>="unknown"<br>25 g |
| DB          | 25577777777777777777777777777777777777                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | നയഗ                                                                    | 0 <del>4</del> 8 0                                                                              | 10 10 10 -                                                                                       | 80<br>41<br>122<br>115<br>67                                                                                                              | പ്ര                                         | റമരപ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 104<br>38<br>80                                       | 74<br>40<br>118<br>110                      |                                                                        | 215)<br>avit<br>s of<br>dise<br>830-                                                                               | on/Qr                            |
| Length      | 215<br>215<br>1245<br>1245<br>1245<br>1388<br>1388<br>1505<br>1505<br>1505<br>17013                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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              | 1165<br>1192<br>1330<br>1330<br>1871                                                                                                      | 4 6 6                                       | 0.00.00.00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 100                                                   | 4800                                        | 2.<br>5 from                                                           | iclassified. (classified. (bases 1 to 215) nnett,A., Labavit ant inhibitors of nntrol fungal dise tent: US 5569830 | Location 1.215/organ             |
| Query       | <br>   <br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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| Score       | 894696969696                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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387 caaggccctgaaggagggcaagtcggtggacaagcccatctacaaccacgtgtccg 442
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Best Local Similarity 76.1%;
Matches 35; Conservative
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nes 39; Conservative
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                               [ (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
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Zauner, W. Kratz, J., Staunton, J., Feick, P. and Wiche, G.
Identification of two distinct microtubule binding domains on recombinant rat MAP 18
Dur. J. Cell Biol. 57 (1), 66-74 (1992)
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    Score 28; DB 57; Length 215;
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                                    55; Mismatches 55; Indels
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                    Pred. No. 7.95e-05;
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Sequence 5 from patent US 5569830.
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Best Local Similarity 17.0%;
Matches 23: Constant
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Best Local Similarity 12.8%;
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YTALAPEADNYDLMYNGVKALKEGKSVDKPTYNHVSGLIDAPEKISSPPILVIEGLHP
YYAKLAPEADFNIYLDSDIKFWRYIORDMARGHSISSIKSIRARRDPDAYID
POKKRABAILQVLPOLVPDDKGQYLLAVRLIMKEGSKMFDPVYLFDEGSTISNIPGGR
KLTGSFPGIKMFYGPDTWYGQEVSVLEMDGGFDKLEELIYVESHLSNTSAKFYGEITG
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/db_xref="PID:9167432"
/translation="MAFTMRAPAPRATAQSRVTANRARRSLVVRADKDKTVV1GLAAD
Direct Submission
Submitted (07-AUG-1991) G. Wiche, Inst of Biochemistry, University
of Vienna, Wachringerstrasse 17, 1090 Vienna, AUSTRIA
revised by [3]
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Chlamydomonas reinhardtii
Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Chlorophyta;
Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
I to 16 bases 1 to 1245)
Roesler, K. R. and Ogren, W.L.
Chlamydomonas reinhardtii phosphoribulokinase: Sequence,
purification and kinetics
Plant Physiol. 93, 188-193 (1990)
Location/Qualifiers
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Wiche,G.
Wintect Submission
Submitted (07-AUG-1992) G. Wiche, Institute of Biochemistry and Molecular Biology, University of Vienna, Dr. Bohrgasse 9, 1030
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C.reinhardtii phosphoribuloKinase mRNA, complete cds.
M36123
g167431
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Pred. No. 6.05e-02;
0; Mismatches 11; Indels
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/codon_start=1
/product="phosphoribulokinase"
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/product="SP17"
| Decourt="PD: 9179084" | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | April 2007 | Ap
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1048..1244
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Submitted (21-3AN-1993) O'Rand M. G., University of North Carolina at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel Hill, North Carolina, USA, 27599-7090
revised by [3] MAT
3 (bases I to 1256)
O'Rand,M.G.
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Submitted (29-APR-1994) O'Rand M. G., University of North Carolina
at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel
Hill, North Carolina, USA, 27599-7090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrata; Eutheria: Lagomorpha; Leporidae; Oryctolagus.

1 (bases 1 to 1256)
Richardson,R.T., Yamasaki,N. and O'Rand,M.G.
Sequence of a rabbit sperm zona pellucida binding protein and localization during the acrosome reaction
Dev. Biol. 165 (2), 688-701 (1994)
                                                                                                                                                                                     02-MAR-1995
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Oryctolagus cuniculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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Pred. No. 1.31e+00;
0; Mismatches 17; Indels
                                                                                                                                                                                         MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryctolagus cuniculus"
/strain="New Zealand white"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="testis"
/cell_type="spermatogenic"
/clone_lib="Rabset"
/clone="SR-16R-16"
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                                                                                                                                                                                     RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
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                                                                                                                                                           O.cuniculus SP17 gene.
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2 (bases 1 to 1256)
O'Rand,M.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 5.0%;
Best Local Similarity 69.6%;
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                          SP17 gene.
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Unpublished
3 (bases 1 to 1388)
Powell,E.E., Wicker,L.S., Peterson,L.B. and Todd,J.A.
Allellc variation of the type 2 tumor necrosis factor receptor gene
Mann. Genome 5 (11), 726-727 (1994)
                                                                                                                                                                        Cases 1 to 1388)

Powell, E.E.

Direct Submission

Submitted (26-NOV-1993) E.E. Powell, c/o John Todd, Level 6

Nuffield Dept of Surgery, The John Radcliffe Hospital, Oxford, UK

( pases 1 to 1388)

Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A.

Amino acid variation in the tumor Necrosis factor receptor 2 is
                                                                                                                         Eukaryotae; mitochondrial eukaryotes; metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
     17-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="murine tumour necrosis factor receptor 2"
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/note="Ser to Thr"
/replace="c"
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   ROD Factor receptor 2 mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="4 (distal region)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                     tumour necrosis factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/note="Ser to Phe"
/replace="t"
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/replace="a"
MMTNFR2A 1388 bp RN
M.musculus tumor necrosis
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/replace="c"
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/replace="c"
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260
                                                                                                            Mus musculus
                                                                                      house mouse.
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95178848
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                DEFINITION
                                                                                                      ORGANISM
                                                                                                                                                                            REFERENCE
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MEDLINE
                                   ACCESSION
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                                                                     KEYWORDS
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                                                                                       SOURCE
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SSTDVCRPHRICSILAIPGNASTDAVCAPESPTLSAIPRILYVSQPEPTRSQPLDQEP
GPSQTPSILTSLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCFILVQRKKK
PSCLQRDAKVPHVPDEKSQDAVGLEQQHLLTTAPSSSSSSLESSASAGDRRAPPGGHP
                                                                                                                   QARVMAEAQCSQEARASSRISDSSHSSHGTHVNVTCIVNVCSSDHSSQCSSQASATV
GDPDAKPSASPKDEQVPFSQEECPSQSPIETTETLQSHEKPLPLGVPDMGMKPSQAGW
VCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTT
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 tcagatgtgctgctgaagtgtcctcctggccaatatgtgaaacatttctgcaacaagac 167
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1 (bases I to 1505)
Lewis, M., Tartaglia, L.A., Lee, A.L., Bennett, G.L., Rice, G.C.,
Tewis, M., Chen, E.Y. and Goeddel, D.V.
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DEFINITION MOUSE tumor necrosis factor receptor 2 mRNA, complete cds.
ACCESSION M60469
                                                                                                                                                                                                                                             /gene="murine tumour necrosis factor receptor 2"
/note="Ser to Thr"
/replace(278,*t")
/gene="murine tumour necrosis factor receptor 2"
/note="Thr to Ile"
/note="Thr to Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Thr to Cys"
replace(1317, "g")
/gene="murine tumour necrosis factor receptor 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="murine tumour necrosis factor receptor 2"
/note="Phe to Ile"
replace(921,"c")
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/note="Ser to Phe"
replace(1047,"t")
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/gene="murine tumour necrosis factor receptor
/note="silent"
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/gene="murine tumour necrosis factor receptor
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Pred. No. 1.31e+00;
0; Mismatches 28; Indels
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                                                                                                                                                                                                                      replace(260, "c")
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417 c 3
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Best Local Similarity 64.1%;
Matches 50; Conservative
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                                                                                                                                                                                            FDQIAVKVA
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Powell,E.E., Wicker,L.S., Peterson,L.B. and Todd,J.A.
Allelic variation of the type 2 tumor necrosis factor receptor gene
95178848
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//codon_start=1
//Lonsolation="Indiagold"
//Lranslation="Indiagold"
//Lranslation
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Nuffield Dept of Surgery, The John Radcliffe Hospital, Oxford, UK
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A.
Amino acid variation in the tumor Necrosis factor receptor 2 is
linked to autoimmune diabetes in NOD mice
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/note="Thr to Cys"
/replace="g"
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/note="silent"
                                /gene="murine tumour necrosis factor receptor 2"
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/replace="t"
1173
                                                                 /note="silent"
/replace="t"
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/replace="a"
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1 (bases 1 to 1388)
Powell, E.E.
Direct Submission
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TITLE
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REFERENCE AUTHORS

JOURNAL MEDLINE

FEATURES

CDS

JOURNAL

JOURNAL REFERENCE

TITLE

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ACCESSION

ORIGIN

οy g δλ KEYWORDS

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TDQVEIRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKGGPGFGVASSRAPNGN
VLCKACAPGTESDTTSSTDVCRPHRTCSILAIPGNASTDAVCAPESPTLSAIPRILY
SQPEPTRSQPLDQEPGPSQTPSILTSTGSTPILISOSTKGGISLDIGILVGVTSLGLLM
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SASAGDRRAPPGGHPQARVMAEAQGPCEARASRISDSSHGSHGSHGTHVNVTCIIVNCSS
SDHSSQCSSQASATVGDPDARPSASPKDEQVPFSQEECPSQSPCETTETLQSHEKPLP
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/db_xref="PID:g202095"
/translation="MAPAALWVALVFELQLWATGHTVPAQVVUTPXKPEPGYECQISQ
                                                                                                                                                                                                                                                   /product="murine tumor necrosis factor receptor 2"
Ab_xxef="PID:g199888"
/translation="MARPAALWELQLWATGHTVPAQVVL_PPXREEPGYECQISQ
EYYDKRAQMCCARCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCT
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
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Goodwin,R.G., Anderson,D.M., Jerzy,R., Davis,T., Brannan,C.I.,
Copeland,N.G., Jenkins,N.A. and Smith,C.A.
Molecular cloning and expression of the type 1 and type 2 murine
receptors for tumor necrosis factor
Mol. Cell. Biol. 11, 3020-3026 (1991)
  Cloning and expression of cDNAs for two distinct murine necrosis
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Murine tumor necrosis factor I receptor (TNFR-1) mRNA, complete
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Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834 (1991)
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Mus musculus lymphoid cDNA to mRNA.
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/cell_type="helper T-cell"
                                                                                                                              /organism="Mus musculus"
41..106
/codon_start=1
41..1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGVPDMGMKPSQAGWFDQIAVKVA
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                                                                                          Location/Qualifiers
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SOURCE
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ILPEMEGLSEFTEYLSESVEVPSPFDILEPPTSGGFLKLSKPCCYIFPGGRGDSALFA
VGFNMLINGGGSERKSCFWKLIRHLDRVDSILLTHGDDDLFPGINSMLGRKIAELEEE
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MKPEPLERSVGNTIEPPVILFOKMGVGKLEMYVLNPVRSSKEMQYFMOQMTGINKDKAR
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SDHSSQCSSQASATVGDPDAKPSASPKDEQVPFSQEECPSQSPCETTETLQSHEKPLP
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                    IDQVEIRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGN
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ETVTEEHLRRAIGNIELGIRSWDINLIECNLDQELKLFVSRHSARFSPEVPGQKILHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (09-JAN-1990) Cowan N.J., Dept. of Biochemistry, New York
University Medical Center, 550 First Avenue, New York, NY 10016
(Dass I to 7620)
Noble, M., Lewis, S.A. and Cowan, N.J.
The microtubule binding domain of microtubule-associated protein
MAPIB contains a repeated sequence motif unrelated to that of MAP2
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EYYDRKAQMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSC1
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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MOUSE MAPIB mRNA for MAPIB microtubule-associated protein.
X51396
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                                                                                                                                                                                                                                                               /product-"tumor necrosis factor receptor 1" 1052 c 981 g 900 t
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                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 28; Indels
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J. Cell Biol. 109 (6 Pt 2), 3367-3376 (1989)
90094539
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                                                                                                                                                                                                                                                                                                                                                                       Score 22; DB 90;
Pred. No. 1.31e+00;
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/db_xref="SWISS-PROT:P14873"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="primary transcript"
                                                                                                                                                                    LGVPDMGMKPSQAGWFDQIAVKVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Swiss Webster"
/dev_stage="5 day old"
/tissue_type="brain"
/clone_lib="lambda GEM"
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                                                                                                                                                                                                                     /gene="TNFR-1"
                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 ctcggacaccgtgtgtgc 272
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 64.1%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 GTGGAAGACCGTGTGCGC 188
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1 (bases 1 to 8818)
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                                                                                                                                                                                                mat_peptide
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ACCESSION
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JOURNAL
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TITLE
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LIEDEEKLKETQPGEAYVIQKETEVSKGSAESPDGGITTTEGEGECEQTPEELEPVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YYEKTERTIKSPCDSGYSYETIEKTTKTPEDGGYTCEITEKTTRTPEEGGYSYEISEK
TTRTPEVSGYTYEKTERSRRLLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSPPES
ESYSYETSTKTTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTTEKKSPSEARQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OOGRQCDETPPISVSESAPSQTDSDVPPEIEECPSITADANIDSEDESETIPTDKTVT
YKHMDPPPAPMQDRSPSPRHPDVSMVDPDALAVDQNLGKAVKKDLKEKTKTKKPGTKT
EVTKTSQVEKTPKVESKEKVLVKKDKPVKTESKPSVTEKEVSSKEEQSPVKAEVAEKQ
                                                                                                               KKEIKKEERKELKKEVKKETPLKDAKKEVKKEEKKEVKKEEKEPKKEIKKISKDIKKS
                                                                                                                                                                                                                                                                                                                                             QGVDDIEKFEDEGAGFEESSETGDYEEKAETEEAEFPEEDGEDNASGSASKHSPTEDD
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SKNVDVEFFKRVRSSYYVVSGNDPAAEEPSRAVLDALLEGKAQWGSNMQVTLIPTHDS
                                                                                                                                                                                                                                                                                                                                                                                                       ESAKAEADVHLKEKRESVVSGDDRAEEDMDDVLEKGEAEQSEEEGEEEDKAEDAREEG
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Human microtubule-associated protein 1B (MAPIB) gene, complete cds.
                                                          ATESKPKVTKDKVVKKEIKTKLEEKKEEKPKKEVVKKEDKTPLKKDEKPRKEEVKKE
                                                                                                                                                                         TPQSDTKKPSALKPKVAKKEESTKKEPLAAGKLKDKGKVKVIKKEGKTTEAAATAVG1
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1 (bases 1 to 9416)
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Pred. No. 1.31e+00;
0; Mismatches 12; Indels
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166..>7629
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Best Local Similarity 73.9%;
Matches 34; Conservative
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Unpublished (1993)
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Homo sapiens
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BASE COUNT

/note="transcription start at bp 166" /product="microtubule-associated protein 1B" 223..7629

/gene="MAP1B"

CDS

/qene="MAP1B"

source

FEATURES

mRNA

TITLE JOURNAL

REFERENCE

AUTHORS

DEFINITION

LT

염 δy ACCESSION

KEYWORDS

ORGANISM

/codon\_start=1 /product="microtubule-associated protein 1B" /db\_xref="PID:g473431"

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VGTGATTAAVWAAGIAAIGPAKELBAERSIMKSPELLIKUPEELIKREEVUNTKOIRA
VLELI EDEEKIKETEPVEAVUOKRREVTKOPAESPDEGITTTEGEGECEGTPEELEP
VLELI EDEEKIKETEPPEGAGFEESSETGODY EEKAETEBAERPEEDEGEEHVOVSAKKHSPT
EDEESAKARADAY IREKRESVASGODKRAEDHOMDA IEKGEBAGOSEERADEEDKAEDA
EDEESKARADAAY IREKRESVASGODKRAEDHOMDA IEKGEBAGOSEERADEEDKAEDAR
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Bugert, P. and Geider, K.
Molecular analysis of the ams operon required for exopolysaccharide synthesis of Erwina amplovora
Mol. Microbiol. 15 (5), 917-933 (1995)
                                                                                                                                                                                                                                                                                                      ATDVKPKAAKEKTVKKETKVKPEDKKEEKERPKKEVAKKEDKTPIKKEEKPKREEVKK
EVRKEIKKEEKKEPKKEVKKETPPKEVKKEVKKEEKEVKKEEKEPKKEIKKIPKDAK
KSSTPLSEAKKPAALKPKVPKKEESVKKDSVAAGKPKEKGKIKVIKKEGKAAEAVAAA
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ILPEMEGLSEFTEYLSESVEVPSPFDILEPPTSGGFLKLSKPCCYIFPGGRGDSALFA
                                                                                                                                      QSQGSTTNSDWMKNLISPDLGVVFLNVPENLKNPEPNIKMKRSIEEACFTLQYLNKLS
MKPEPLFRSVGNTIDPVILFQKMGVGKLEMYVLNPVKSSKEMQYFWQQWTGTNKDKAE
                                                                                                                                                                                                          FILPNGQEVDLPISYLTSVSSLIVWHPANPAEKIIRVLFPGNSTQYNILEGLEKLKHL
DFLKQPLATQKDLTGQVPTPVVKQTKLKQRADSRESLKPAAKPLPSKSVRKESKEETP
                                                                                                                                                                                                                                                                             EVIKVNHVEKPPKVESKEKVMVKKDKPVKTEIKPSVIEKEVPSKEEPSPVKAEVAEKQ
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STASVATSSFPEPTTDDVSPSLHAEVGSPHSTEVDDSLSVSVVQTPTTFQETEMSPSK
EECPRPMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEQSLAMDFSRQSPD
RSDVLETVVLINPSDEAVSTEVRLMITDAARHKLLVLTGQCFENTGELILQSGSFSFQ
                                                                                                   VNGFNMLINGGSERKSCFWKLIRHLDRVDSILLTHIGDDNLPGINSMLQRKIAELEEE
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TNNEETESPSQEFVNITKYESSLYSQEYSKPADVTPLNGFSEGSKTDATDGKDYNASA
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EASPSISSAHTPSQIASPLQEDTLSDVAPPRDMSLYASLISEKVQSLEGEKLSPKSDI
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EARQDVDLCLVSSCEYKHPKTELSPSFINPNPLEWFASEEPTEESEKPLTQSGGAPPP
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THDSEVMREWYQETHEKQQDLNIMVLASSSTVVWQDESFPACKIEL"
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Pred. No. 1.31e+00;
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Local Similarity 73.9%;
nes 34; Conservative
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TGIPQHELDLKIATHILLSVICVGWFWVRLRHYTYRKPFWFELKEVFRTILIFSIVDL
SVSALSKWELSRWIWILTWLLSMAMVPFGRACVKRLLNRKKLWKKQSIIIGSGKNAQE
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DIDKYVNIFFPLIPSLVERMKRKVPKAAANATLGERLOMYETRIGVGDLMYTWHDFB
LITPRAGOXRASASTGRWVHSDGTIFYPYIGRYRYGHTVQETREDEIDSRLSKLYVESPO
VDVNVASFKSQKTYVTGEVTTSGQQAIINVPLTILDAINAAGGLIATADWRNVVLTHD
GROPYVSLAGALMQNDPSQNHLLYPODILYVPRNDEKYFWGEVKQATLKMDRSGM
TLSBALGSAGGMDQXNDATGVFVYIRPWGARRSNIANIYQLITKMDRSGM
TLSBALGSAGGMDQXNDATGVFVYIRPWGARRSNIANIYQLITKMAAMVMGTEFRL
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ADETASIVANEHGVSLQDHVAQQLTADMCRDSDLILWHKKHIDLVCRINPSVRGKTM
LFGHWINQQEIADPYKKSRDAFEAVYGVLENAAQKWVNALSR"
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VVADMGKDTGVLGLTYSGEDPVQISRVLDQVINNYLYQNIARKSEEAEKSIQFLAQQL
PDVRAKLDQAEDKLNVFRRKHDSVDMSLEAKSALDSSVSIQTQLNALTFREAEVSQLF
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TVADLGLDVLVQQDHFPLIGAGLSRIIGQKAQQIAVSRLKVPTLMDKRELSVEVDGPD
                                                                                                                                                                        Submitted (01-MAR-1994) K. Geider, MPI fuer medizinische Forschung, Jahnstr 29, 69028 Heidelberg, FRG
3 (bases 1 to 17013)
Geider, K.K.
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/db_xref="PID:9600427"
                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (06-DEC-1994) K.K. Geider, MPI fuer medizinische
Forschung, Jahnstr 29, 69028 Heidelberg, FRG
Location/Qualifiers
1..17013
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/db_xref="PID:g600430"
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/db_xref="PID:9600428"
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/db_xref="PID:9600429"
/transl_table=11
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/gene="amsH"
/codon_start=1
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/gene="ams1"
/codon_start=1
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/gene="amsG"
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/gene="ams1"
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HGIDNPEQLEELGLUVYASYPELSEWGRKDOETLLTANDAYVAYSVELYLAKGIFH
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YKRFIQUGIDIKGIILNAVVRKSANNYGYGYDYYDYSYQQGEKS"
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LINKDNRNDFLKRLMNKLRTRLTGK"
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RKGIMKEDRFVYILLIAYSIGAAVRITFSDPSÍFGGRYGNLFHTEPLLFAFLAMIRIR
NILLNFFMLFSITTYYLAYNTILSAPSIMGYSVAPLFRIS"
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YSRLICCOHVSIETLSAAVRKLKVEYGLAEXVVVLTOHDIMVXLTASFSLKNYVVS
NISPFHENSLNRFDDARAKONRVLAVGRLTYQKNFGRLLDIMVNHKQGWKLLIVG
DGEEKAELLEKIKKHLEESARIVSPSKRISBYRSSGVIAMTSRYEGLEMVLIEARN
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QQELNISKASTVGDVRIIDHAETAAKPVAPKSILIVAGSLILGLVVSVGLVLMKALFH
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9775..10575
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Matches 42; Conservative
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              TIASSGODEHWRRVSDDMNRITLEPDFGAVADGKKDCLPAVMANYHWAQNINNQKLSIQF
PAGREPISSPDISAKYIRFLRLAGAPVHCGYEPATTLASDGKSEFLEKVNARWYELSN
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MNFGTPAVAINYEHKSLGYWKQLGLPEMASDVQSLMDGSIIAKVKGVLDNYEEMEQQV
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SKLLLPAIVAANKKPFAADIFLVHFGYAGALANKLRELKVLQGKQVTVFHGADISRRH
ILEEHKKDYPRLFAQNELLLPISRLWGHKLIAMGCPAEKINVTRMGIEPEKFNLKLRD
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                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKILLVGNHTCGNRGDGAILRGIIDSLHLERTDLDIDIISRFPT
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Chlamydomonas reinhardtii 8 kDa outer arm dynein light chain mRNA,
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Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlorophyceae; wicochondrial eukaryotes; Viridiplantae; Chlorophyta;
Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 683)
The Mrx) = 8,000 and 11,000 cuter arm dynein light chains from Chlamydomonas flagella have cytoplasmic homologues
Chlamydomonas flagella have cytoplasmic homologues
5. Biol. Chem. 270 (19), 11445-11452 (1995)
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14283..14286
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13042..14289
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ANQYTAALNPILFXVLISPMLGGTTDGKVVDENLERLKKKVLEVYEARLTKCKYLAGDF
LSLADLNHVSYTLCLFATFYASVLDAYPHYRAWWSGLMERPSYVQKVAALMKPGA"
                                                                                                                                /clone_lib="lambda ZAPII cDNA made from cells regenerating
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1 (bases 1 to 1671)
Shah,D.M., Hironaka,C.M., Wiegand,R.C., Harding,E.I., Krivi,G.G. and Tiemeier,D.C.
Structural analysis of a maize gene coding for glutathione-S-transferase involved in herbicide detoxification
Location/Qualifiers
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Maize glutathione S-transferase gene (GST-I), exons 2 and 3.
M16902
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join(M16900:246..395,238..286,956..1401)
/note="glutathione S-transferase I"
/organism="Chlamydomonas reinhardtii"
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Pred. No. 5.68e+00;
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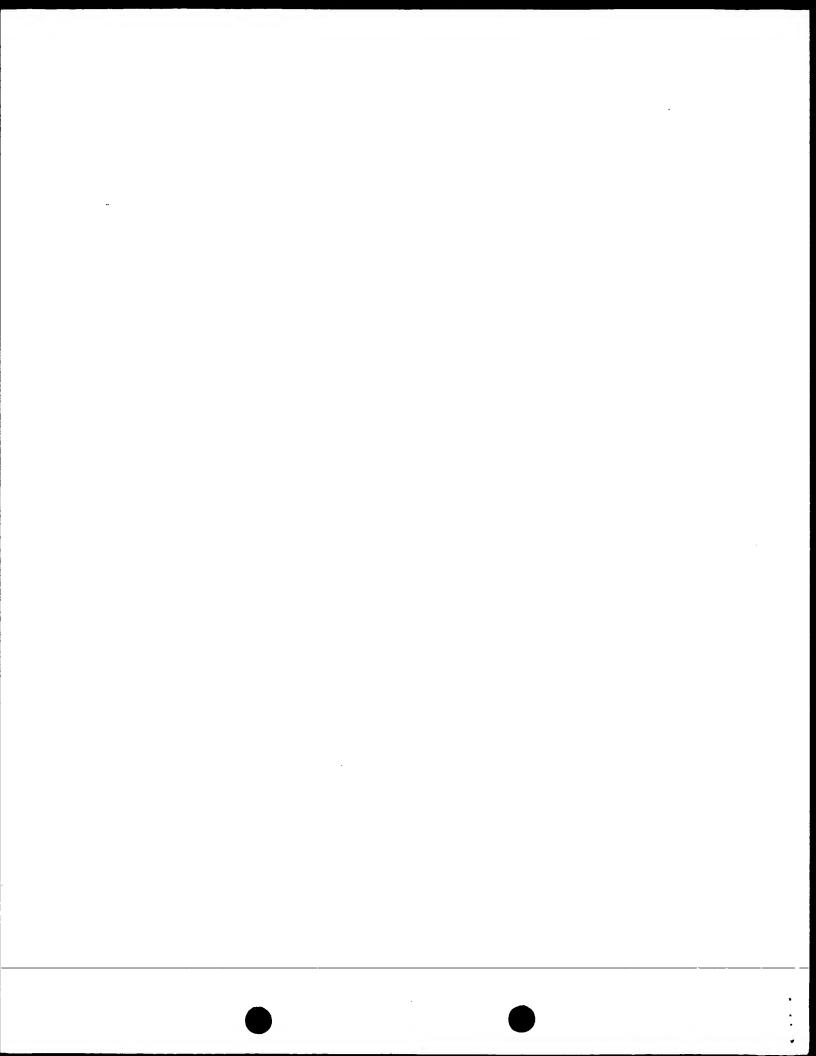
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93..1865
/note="muscarinic acetylcholine receptor III (AA 1 - 590)"
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Akiba,I., Kubo,T., Maeda,A., Bujo,H., Nakai,J., Mishina,M. and Numa,S.
Primary structure of porcine muscarinic acetylcholine receptor III and antagonist binding studies
FEBS Lett. 235 (1-2), 257-261 (1988)
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Best Local Similarity 78.4%; Pred. No. 5.68e+00;
Matches 29; Conservative 0; Mismatches 8; Indels
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Data kindly reviewed (03-OCT-1989) by Numa S.
Location/Qualifiers
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Gaps ô Match 4.8%; Score 21; DB 48; Length 1913; Local Similarity 83.9%; Pred. No. 5.68e+00; es 26; Conservative 0; Mismatches 5; Indels Query Match kest Local Si Matches 26

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Search completed: Tue Dec 2 17:21:44 1997 Job time : 415 secs.



| *                                       |      | *                                       |
|-----------------------------------------|------|-----------------------------------------|
| * * *                                   | (TM) | ****                                    |
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

- n.a. database search, using Smith-Waterman algorithm п .а MPsrch\_nn Tue Dec 2 17:22:01 1997; MasPar time 56.86 Seconds 803.956 Million cell updates/sec Run on:

alar output not generated

>US-08-915-004-14 (1-438) from US08915004.seq 438 Description: Perfect Score: tle:

......AGCCACAGATATGTATCTGA 438 1 ATGAACAAGTTGCTGTGCTG. TACTTGTTCAACGACACGAC. Sequence:

N.A.

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD : Nmatch

142080 seqs, 52183452 bases x Searched:

Listing first 45 summaries Minimum Match Post-processing:

n-geneseg28 Database:

i.parti i.part2 3.part3 4.part4 5.part5 6.part6 7.part7
8.part8 9.part9 10.part10 11.part11 12.part12 13.part13
14.part14 15.part15 16.part16 17.part17 18.part18
19.part19 20.part20 21.part21 22.part22 23.part23
24.part24 25.part25 26.part26 27.part27 28.part28

Mean 8.240; Variance 4.524; scale 1.822 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result<br>No. | Score | Query<br>Match | Length DB | DB | ΩI     | Description           | Pred. No. |
|---------------|-------|----------------|-----------|----|--------|-----------------------|-----------|
| -             | 438   | 100.0          | 438       | 28 | T36689 | Osteoclastogenesis in | 0.00e+00  |
| 7             | 402   | 91.8           | 1173      | 78 | T35475 | Human tumour necrosis | 4.15e-284 |
| m             | 400   | 91.3           | 432       | 27 | T33176 | Mutated OCIF, OCIF-CC | 1.48e-282 |
| 4             | 400   | 91.3           | 564       | 27 | T33180 | Mutated OCIF, OCIF-CB | 1.48e-282 |
| 2             | 400   | 91.3           | 594       | 27 | T33175 | Mutated OCIF, OCIF-CD | 1.48e-282 |
| 9             | 400   | 91.3           | 819       | 27 | T33174 | OCIF, (               | 1.48e-282 |
| 7             | 400   | 91.3           | 996       | 27 | T33179 | Mutated OCIF, OCIF-CS | 1.48e-282 |
| 80            | 400   | 91.3           | 186       | 27 | T33170 | Mutated OCIF, OCIF-DD | 1.48e-282 |
| σ             | 400   | 91.3           | 984       | 27 | T33171 | Mutated OCIF, OCIF-DD | 1.48e-282 |
| 10            | 400   | 91.3           | 1056      | 27 | T33173 | Mutated OCIF, OCIF-CC | 1.48e-282 |
| 11            | 400   | 91.3           | 1080      | 27 | T33169 | Mutated OCIF, OCIF-DC | 1.48e-282 |
| 12            | 400   | 91.3           | 1182      | 27 | T33178 | Mutated OCIF, OCIF-CB | 1.48e-282 |
| 13            | 400   | 91.3           | 1200      | 27 | T33172 | Mutated OCIF, OCIF-CL | 1.48e-282 |
| 14            | 400   | 91.3           | 1206      | 27 | T33164 | Mutated OCIF, OCIF-C2 | 1.48e-282 |
| 15            | 400   | 91.3           | 1206      | 28 | T36685 | Osteoclastogenesis in | 1.48e-282 |

Query Match
100.0%; Score 438; DB 28; Length 438;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;

| 8.83e-28           | C2 5.27e-281 | C2 5.27e-28 | Cl 5.27e-28 | C2 5.27e-28 | I 7.59e-26           | C 4.44e-21 | C 5.43e-21 | 3.81e-16    | oc 1.91e-13 | 5e-11      | 1.36e-1 | .36e-1 | 5.65e-1             | 1.10e-1               | 9.9<br>9.9          | 30 8.90e-1 | e 3.77e-0            | e 3.77e-0            | 3.77e-0              | 1.58e-0              | e 6.57e-0            | e 2.70e-0            | e 2.70e-0            | e 2.70e-0            | e 1.09e-0            | e 1.09e-0 | 1.09e-0              | 4.37e-0  | 1.73e-0              |
|--------------------|--------------|-------------|-------------|-------------|----------------------|------------|------------|-------------|-------------|------------|---------|--------|---------------------|-----------------------|---------------------|------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|-----------|----------------------|----------|----------------------|
| Osteoclastogenesis |              |             |             |             | Fragment of human OC | OCIF       | CIF, OCIF- | OCIF, OCIF- | OCIF-       | OCIF, OCIF | etic    | υ      | Base substituted E. | Oligonucleotide probe | Oligonucleotide pro | ы          | Generic DNA sequence | Generic DNA sequence | Generic DNA sequence | Generic DNA sequence | Generic DNA sequence | Generic DNA sequence | Generic DNA sequence | Generic DNA sequence | Generic DNA sequence | c DNA s   | Generic DNA sequence | ic DNA s | Generic DNA sequence |
| 999                | T33162       | 316         | 316         | 316         | 318                  | 317        | 316        | 318         | 316         | 316        | 057     | 057    | 116                 | 174                   | 051746              | 116        | 047                  | 046                  | 04                   | 046                  | 9                    | 04                   | 046                  | 04                   | 047                  | 04        | 046                  | 04       | 070471               |
| 28                 | 28           | 27          | 28          | 27          | 27                   | 27         | 27         | 27          | 27          | 27         | ~       | 7      | Н                   | σ                     | σ                   | Н          | 12                   | 12                   | 12                   | 12                   | 12                   | 12                   | 12                   | 12                   | 12                   | 12        | 12                   | 15       | 12                   |
| 465                | 1206         | 20          | 20          | 1206        | 13                   | 321        | 1080       | 255         | 08          | 1080       | 9       | 1047   | 204                 | 91                    | 91                  | 204        | 114                  | 114                  | 114                  | 114                  | 114                  | 114                  | 114                  | 114                  | 114                  | 114       | 114                  | 114      | 114                  |
|                    | σ.           |             |             |             |                      |            |            |             |             |            |         |        |                     |                       |                     |            |                      |                      |                      |                      |                      |                      |                      |                      |                      |           |                      |          |                      |
| 91                 | 06           | 90          | 90          | 8           | 84                   | 72         | 71         | 55          | 48          | 42         | 10      | 10     | σ                   | σ                     | ω                   | Φ          | æ                    | œ                    | ω                    | 8                    | 7                    | 7                    | 7                    | 7                    | 7                    | 7         | 7                    | 7        | φ                    |
| 6                  | 398          | σ           | σ           | σ           | ~                    | Н          | $\vdash$   | 4           | Н           | æ          | 46      | 46     | 42                  | 40                    | 37                  | 37         | 36                   | 36                   | 36                   | 35                   | 34                   | 33                   | 33                   | 33                   | 32                   | 32        | 32                   | 31       | 30                   |
| 16                 | 11           | 18          | 13          | 20          | 21                   | 22         | 23         | 24          | 25          | 56         | 27      | 28     | 53                  | 30                    | 31                  | 32         | 33                   | 34                   | 35                   | 36                   | 37                   | 38                   | 33                   | 40                   | 41                   | 42        | 43                   | 44       | 45                   |
|                    |              |             |             |             |                      |            |            |             |             |            |         | υ      |                     |                       | U                   | O          |                      |                      |                      |                      | υ                    |                      |                      | υ                    |                      | U         | U                    |          |                      |

# ALIGNMENTS

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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 24; Page 76; 183pp; Japanese.
This sequence encodes full length osteoclastogenesis inhibitory factor (OCIF) 5. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducting conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                     22-APR-1997 (first entry)
0steoclastogenesis inhibitory factor 5 coding sequence.
0steoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
                                                                                                                                                                                                                                                                                    Morinaga
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                    29-AUG-1996.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 C;
                                                                                                           Location/Qualifiers 1..63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 A;
 BP
 standard; DNA; 438
                                                                                                                                                         64..435
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                                                                                                                                                                                                                                                                                                                                 P-PSDB; W99930
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                                                                                             Homo sapiens
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                                                                                                                                          /*tag= a
mat_peptide
                  T36689;
T36689
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 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human tumour necrosis factor receptor - used to develop prods.

To treating e.g. tumours, infection, auto:immune disease, graft rejection, cytotoxicity or inflammation

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

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Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 59pp; English

Claim 1; Fig 1; 5pp; English

Claim 1; Fig 1; 5pp; English

Claim 1; Fig 1; 5pp; English

Claim 1; Fig 1; 5pp; English

Claim 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fig 1; Fi
                                                                                                                                                                                                                                                    gtgtgcgcccttgcctgaccactactacacagacagctggcacaccagtgacgagtgt 240
                                                                                                                               caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
                                                                                                                                                                                    igtgacaaatgtcctcctggtacctacctaaaaacaacactgtacagcaaagtggaagacc 180
                                                                                                                                                                                                         GTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                            CACAACCGCGTGTGCGAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cataggagctgccctcctggatttggagtggtgcaagctggatgcaggagaagacccaag 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atgaacaagttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAY-1997 (first entry)
Human | tumour necrosis factor receptor.
Tumour necrosis factor, TNF, receptor; TNF-beta; ligand; tumour;
differentiation; immune response; autoimmune disease; inflammation;
septic shock; graft-versus-host; apoptosis; ss.
                                                                                                                                                                                                                                                                                                                                 GIGIGCGCCCTTGCCCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                           ¢acaaccgcgtgtgcgaatgcaaggaagggcgctaccttgagatagagttctgcttgaaa
 0; Indels
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T35475 standard; cDNA; 1173 BP.
T35475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-1995; ZA-002587.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACAGATATGTATCTGA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccacagatatgtatctga 438
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 Conservative
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15-MAR-1995; U03216.
15-MAR-1995; WO-U03216.
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WPI; 96-433821/43.
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P-PSDB; R99357
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Matches
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1D T3
AC T3
AC T3
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EW TC
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KW d2
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OS HC
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To the needing osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis olaim 72; Page -; 183pp; Japanese.

Claim 72; Page -; 183pp; Japanese.

Claim 72; Page -; 183pp; Japanese.

Claim 72; Page -; 183pp; Japanese.

Claim 72; Page -; 183pp; Japanese.

Costeoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CCR4 in which amino acids 123·380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under reducing conditions. The protein is adsorbed onto cation-exchangers non-reducing conditions. The protein is adsorbed onto cation-exchangers or hepstrin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. This sequence is not given in the specification and is derived from the protein sequence and the wild type OCIF CDNA sequence given in T36685.

Sequence 432 BP; 116 A; 117 C; 106 G; 93 T;
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CAGGAAACGITICCICCCAAAGIACCTICAITAIGACGAAGAAACCICICATCAGCIGIIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 tgtgacaaatgtcctcctggtacctacctaaaacaacactgtacagcaaagtggaagacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GIGIGGGCCCCTIGCCCIGACCACIACIACAGAGACAGCIGGCACACCAGTGACGAGIGI 240
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Mutated OCIF, OCIF-CCR4, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
                                                                                                                                                                                                                               1 atgaacaagttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                                                                                                                                                                                                                                                                                                         1 AIGAACAAGIIGCIGIGCIGCGCCCCCGIGIIICIGGACAICICCAIIAAGIGGACCACC 60
                                                                                                                     0; Gaps
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29-AUG-1996, J00374.

R 20-FEB-1995; JP-054977.

PR 21-JUL-1995; JP-207508.

PA (SNOW) SNOW BRAND MILK PROD CO LTD.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

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PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995; JP-207508.

PR A1-JUL-1995
     Score 402; DB 28; Length 1173;
                                                                                                               0; Indels
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                                                                Pred. No. 4.15e-284;
                                                                                                                     0; Mismatches
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T33176 standard; DNA; 432 BP.
ch 91.8%;
1 Similarity 100.0%;
402; Conservative
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/product= OCIF-CCR4
WO9626217-A1.
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Synthetic.
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/*tag= a
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mat_peptide
     Query Match
                                                                Best Local
                                                                                                               Matches
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for bone resorption control, sep. treatment of osteporosis

Claim 84; Page 149-150; 183pp; Japanese.

This sequence encodes a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence encodes OCIF-CBsp in which amino acids 167-380 of the mature
protein have been deleted. These amino acid changes have been caused
by the introduction of a restriction site. The OCIF of the invention
has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
and 120 kD under non-reducing conditions. The protein is adsorbed onto
cation-exchangers or heparin and its activity is lowered after 10 mins
at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
deg.C. OCIF is useful in the control of bone resorption and therefore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 gtgtgcgcccttgccctgaccactactacacagacagctggcacaccagtgacgagtgt 240
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        241
        ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc
        300

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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                           121 tgtgacaaatgtcctcctggtacctacctaaaaacaacactgtacagcaaagtggaagacc 180
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                                                                                                                                                                                                                           caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
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                                                                                                                                                                   1 ATGAACAAGTTGCTGTGCTGCGCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACC 60
                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GTGTGCGCCCCTTGCCCTGACCACTACTACAGAGAGCTGGCAGAGAGTGAGGAGTGT
                                                                                                             1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc
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Yasuda H;
Length 432;
                                                        Indels
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20-FEB-1995; JP-054897.
21-012-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI, 96-402320/40.
Score 400; DB 27; Pred. No. 1.48e-282;
                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 4
T33180 standard; DNA; 564 BP
Query Match
Best Local Similarity 99.8%;
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23-APR-1997 (first_entry)
                                                        401; Conservative
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/*tag= b
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                                                        Matches
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for bone resorption control, esp. treatment of osteoporosis claim 69; Page -; 183pp; Japanese.

Claim 69; Page -; 183pp; Japanese.

Claim 69; Page -; 183pp; Japanese.

Claim 69; Page -; 183pp; Japanese.

Sequence encodes a mutated version of the full length

osteoclastogenesis inhibitory factor (COIF) of the invention. This sequence encodes OCIF-CDD1 in which amino acids 177-380 of the mature protein have been deleted. The OCIF of the invention and 120 kD under veright by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. This sequence is not given in the specification and is derived from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1997 (first entry)
Mutated OCIF, OCIF-CDD1, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                                                                                                                                           Gaps
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                                                          91.3%; Score 400; DB 27; Length 564; 99.8%; Pred. No. 1.48e-282;
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124 T;
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                                                                                                                           Indels
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20-FEB-1996; JO0374.
20-FEB-1995; JP-05497.
21-ULE-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, P-PSDB; R99945.
132 G;
                                                                                                                              0; Mismatches
149 C;
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T33175 standard; DNA; 594 BP.
T33175;
159 A;
                                                                                                                              401; Conservative
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                                                                                                Best Local Similarity
564 BP;
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mat_peptide
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   Sequence
                                                                 Query Match
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                                                                                                                              Matches
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim [66, Page 145; 183pp; Japanese.

This Sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CDD2 in which amino acids 252-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kb under reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 70 mins at 56 deg.C. and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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protein sequence and the wild type OCIF cDNA sequence given in T36685. Sequence 594 BP; 176 A; 152 C; 136 G; 130 T;
                                                                                                                                                                                                                                                               tgtgacaaatgtcctcctggtacctacctaaaacaacatgtacagcaaagtggaagacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-APR-1997 (first entry)
Mutated OCIF, OCIF-CDD2, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                          61 ¢aggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
                                                                                                                       1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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Yasuda H;
                                                        Length 594;
                                                                                      1; Indels
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W09656217-A1.
20-FB46-1996, J00374.
20-FBB-1995, JP-054977.
21-JUL-1995, JP-057508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOTO M, Higashio K, Kobayashi F, Mochizuki S, Mo:
WPI: 96-402320/40.
P-PSDB; R99944.
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                                                    Score 400; DB 27; 1 Pred. No. 1.48e-282;
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                                                Query Match 91.3%;
Best Local Similarity 99.8%;
Matches 401; Conservative
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 81; Page 149; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CSph in which maino acids 298-380 of the mature protein have been deleted and replaced by Ser-Leu-Asp. These amino acid changes have been caused by the introduction of a restriction site. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and
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                                                                                                                                                                                                                                                                                                                        61 caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
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Mutated OCIF, OCIF-CSph, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                       1 atgaacaacttgctgctgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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Yasuda H;
                               / Match 91.3%; Score 400; DB 27; Length 819; Local Similarity 99.8%; Pred. No. 1.48e-282; Local 401; Conservative 0; Mismatches 1; Indels (
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Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
188 G;
198 C;
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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251 A;
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W09626217-A1.
819 BP;
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis claim 5½, Page 141-142; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DDDI in which amino acids 178-252 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C or CIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Osteoclastogenesis inhibitory factor: OCIF; heparin; bone resorption;
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                                                                                                                                                  1 ATGAACAAGTTGCTGTGCTGCGCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACC 60
                                                                                                                               1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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prevention of disorders of bone resorption, e.g. osteoporosis. Sequence 966 BP; 301 A; 228 C; 226 G; 211 T;
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
                                                                         Pred. No. 1.48e-282;
                                                        DB 27;
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T33170 standard; DNA; 981 BP.
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22-APR-1997 (first entry)
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To the product of the control, esp. treatment of osteoporosis claim 57; Page 142-143; 183pp; Japanese.

To bone resorption control, esp. treatment of osteoporosis claim 57; Page 142-143; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes of CIF-DDD2 in which amino acids 253-326 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under reducing conditions and 120 kD under on reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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W9926217-A1.
W9926217-A1.
20-RCB-1996; J00374.
20-RCB-1995; JP-054977.
20-RCB-1995; JP-054977.
21-JUL-1995; JP-05598.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, H1gachlo K, Kobayashi F, Mochizuki S, Mo
WARGAWA N, Shima N, Tsuda E, Ueda M, Yano K, Ya
WPI; 96-401320/40.
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                               Query Match 91.3%; Score 400; DB 27; 1
Best Local Similarity 99.8%; Pred. No. 1.48e-282;
Matches 401; Conservative 0; Mismatches 1;
218 G;
238 C;
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312 A;
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981 BP;
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PF 20-FEB-1996; J00374.

PF 20-FEB-1996; J00374.

PR 20-FEB-1996; JP-03697.

PR 20-FEB-1996; JP-03697.

PR 20-FEB-1996; JP-03697.

PR 20-FEB-1996; JP-03697.

PR 20-FEB-1996; JP-03697.

PR 20-FEB-1996; JP-03697.

PR 20-FEB-1996; JP-03697.

PR 20-FEB-1996; JP-03697.

PR 30-MA Higashio K, Kobayashi F, Mochizuki S, Morinaga T;

PI GOLD M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;

PI GOLD M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;

PI GOLD M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;

PI Saguance accordation control, esp. treatment of osteoporosis

Claim 63; Page 144-145; 183pp; Japanese.

Claim 63; Page 144-145; 183pp; Japanese.

Claim 63; Page 144-145; 183pp; Japanese.

Claim 63; Page 144-145; 183pp; Japanese.

Claim 63; Page 144-145; 183pp; Japanese.

Control of societed a mutated version of the full length costeoprosis

Control of degree of 60 kD under reducing conditions and 120 kD under control of bone resorption and therefore in the treatment and its activity is lowered after 10 mins at 90 degr. Oct 190 control of bone resorption and therefore in the treatment and its needing conditions and 120 kD under control of bone resorption, e.g. osteoporosis.
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Mutated OCIF, OCIF-CC, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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          Score 400; DB 27; I
Pred. No. 1.48e-282;
0; Mismatches 1;
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          91.3%;
99.8%;
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Best Local Similarity 99.8%;
Matches 401; Conservative
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To bone rescription control, esp. treatment of osteoporosis

Control of the page 140-141; 183pp; Japanese.

Control of page 140-141; 183pp; Japanese.

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22-APR-1997 (first entry)
Mutated OCIF, OCIF-DCR4, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                            1 atgaacaacttgctgtgctgcgcgctcgtgttctggacatctccattaagtggaccacc 60
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Yasuda H;
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29-AUG-1996.
20-FEB-1995; JP-054977.
20-FEB-1995; JP-207508.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Mo Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yan P-PSDB; R99939.
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        Score 400; DB 27; L
Pred. No. 1.48e-282;
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        91.3%;
Query Match
Best Local Similarity 99.8%;
Matches 401; Conservative
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91.3%; Score 400; DB 27; Length 1080;

Query Match

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Claim 78; Page 148; 183pp; Japanese.

Claim 78; Page 148; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CBst in which Gla371 is substituted with Leu and amino acids 373-380 of the mature protein have been deleted. These anion acid changes have been caused by the introduction of a restriction site. The OCIF of the invention has a molecular weight by SDS-PAGE of the invention has a molecular weight by SDS-PAGE of the invention has a molecular weight by SDS-PAGE of conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Mutated OCIF, OCIF-CBst, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
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20-FEB-1996; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Pred. No. 1.48e-282;
                     Mismatches
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Nakagawa N, Shima N, Tsuda E, Ueda M,
WPI; 96-402320/40.
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Best Local Similarity 99.8%;
                          401; Conservative
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 60; Page 143-144; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CL in which amino acids 379-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutated OCIF, OCIF-CL, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                   tgtgacaaatgtcctcctggtacctacctaaaacaacactgtacagcaaagtggaagacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                               gigigogoccotigocoigaccactactacagacagacagciggcacagcagtgacgagtgt 240
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                                                                                                           1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                       0; Gaps
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Length 1182;
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                                                       Indels
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21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                                       ij
Score 400; DB 27; 1 Pred. No. 1.48e-282;
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                                                       0; Mismatches
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T33172 standard; DNA; 1200 BP.
T33172;
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Query Match

91.3%;

Best Local Similarity 99.8%;

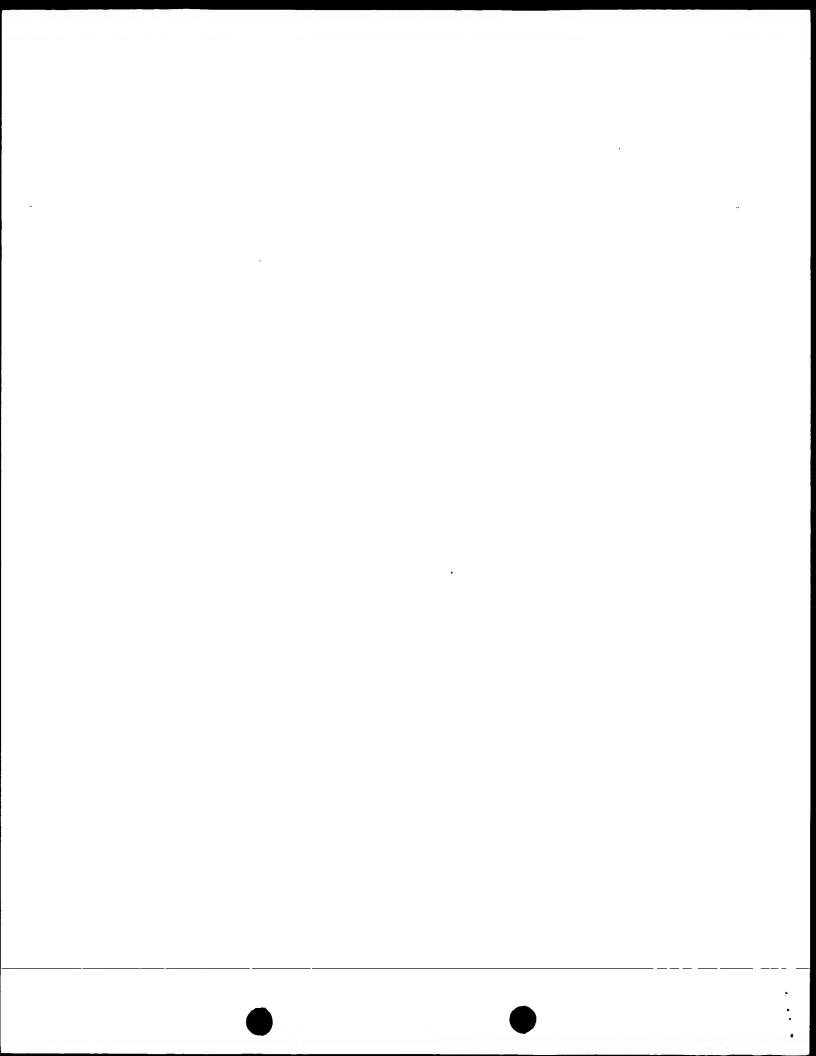
Matches 401; Conservative
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This sequence encodes a mutade version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes to which the 22nd Cys residue in the mature oCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation—exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption of circum the control of bone resorption.
                                                                                                                                                                                                                                                                          9t9t9c9ccccttgcctgaccactactacacagacagctggcacacagtgacgagtgt 240
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Mutated OCIF, OCIF-C22S, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                       àtgaacaacttgctgtgctgcgcgctcgtgttctggacatctccattaagtggaccacc 60
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                      1; Indels
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-20550.8.
(SNOW |) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
P-PSDB; R99934.
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Best Local Similarity 99.8%; Pred. No. 1.48e-282;
                      0; Mismatches
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T33164 standard; DNA; 1206 BP.
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                    401; Conservative
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W09626217-A1.
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                  1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                                                                                                  1 ATGAACAAGTTGCTGTGCTGCGCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACC 60
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N, Shima N, Tsuda E, Ueda M, Yano K,
Best Local Similarity 99.8%; Pred. No. 1.48e-282; Matches 401; Conservative 0; Mismatches 1;
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-ULL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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T36685 standard; DNA; 1206 BP
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WPI; 96-402320/40.
P-PSDB; R99924-25.
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| Q   | п                    | atgaacaacttgctgtgctgcgctcgtgtttctggacatctccattaagtggaccacc 60    |
|-----|----------------------|------------------------------------------------------------------|
| Qy  | Ħ                    | ATGAACAAGTIGCTGTGCTGCGCGCTCGTGTTTCTGGACATCTCCCATTAAGTGGACCACC 60 |
| QQ  | 61                   | caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120 |
| οy  | 61                   | CAGGAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGAACCTCTCATCAGGTGTG 120   |
| qq  | 121                  | tgtgacaaatgtcctcctggtacctacctaaaacaacactgtacagcaaagtggaagacc 180 |
| Qy  | 121                  | TGTGACAAATGTCCTCCTGGTACCTAACACACACTGTACAGCAAAGTGGAAGAC 180       |
| qa  | 181                  | gtgtgcgccctttgccctgaccactactacacagacagctggcacaccagtgacgagtgt 240 |
| Qy  | 181                  | GTGTGCCCCTTGCCCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGT 240   |
| qq  | 241                  | ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc 300 |
| ογ  | 241                  | CTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACC 300 |
|     | 301                  | cacaaccgcgtgtgcgaatgcaaggaagggcgctaccttgagatagagttctgcttgaaa 360 |
| Š   | 301                  | CACAACGGCGTGTGCGAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAA 360 |
| qq  | 361                  | cataggagctgcctcctggatttggagtggtgcaagctgga 402                    |
| Oy  | 361                  | CATAGGAGCTGCCCTCCTGGATTTGGAGTGCAAGCTGGA 402                      |
| Se. | arch com<br>b time : | Search completed: Tue Dec 2 17:23:02 1997<br>Job time : 61 secs. |



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn

Run on:

Tue Dec 2 17:23:26 1997; MasPar time 278.32 Seconds 807.828 Million cell updates/sec lar output not generated.

>US-08-915-004-14 (1-438) from USO8915004.seq 438 ifle: Description: Perfect Score:

......AGCCACAGATATGTATCTGA 438 1 ATGAACAAGTTGCTGTGCTG. TACTTGTTCAACGACACGAC. N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD : Nmatch

707517 seqs, 256659390 bases x Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

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1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8

9:EST9 10:EST10 11:EST11 18:EST12 13:EST13 14:EST14

15:EST9 16:EST10 11:EST11 18:EST13 14:EST14

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Database:

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175:EST175 176:EST176 177:EST177 178:EST178 179:EST179 180:EST180 181:EST181 182:EST182 183:EST183 184:EST184 185:EST186 186:EST186 187:EST187 188:EST188 189:EST189 190:EST190 191:EST191 192:EST192 193:EST194
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Mean 10.031; Variance 1.782; scale 5.629 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| No.   Score   March Length DB   ID   Description   Pred: No.   No.   Score   March Length DB   ID   Description   Pred: No.   No.   Score   March Length DB   ID   Description   Pred: No.   No.   Score   March Length DB   ID   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.      |         | t<br>. Scor | Query |              |          |             |                             |          |
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| 1 23 5.3 344 61 H1106 ym62405.11 Homo sapie 2.49e- 2 2 5.0 300 183 AA100384 za46605.11 Homo sapie 6.10e- 3 2 5.0 475 57 T42477 5740 Arabidopsis thal 6.10e- 5 2 5.0 475 117 M29026 5.0 6.10e- 6 2 5.0 475 117 M29026 5.0 6.10e- 6 2 6 6 10e- 6 6 10e- 7 2 5.0 475 117 M29026 5.0 6.10e- 8 2 1 4.8 325 19 T54964 zk67401.81 Panctara cD 6.10e- 9 2 1 4.8 325 19 T54964 yb24003.11 Homo sapie 1.34e- 11 2 1 4.8 371 99 N61165 Celegans CDNA clone 1.34e- 12 1 4.8 371 99 N61165 Celegans CDNA clone 1.34e- 13 2 1 4.8 376 5.7 77009 yp23005.51 Homo sapie 1.34e- 13 2 1 4.8 376 5.7 77009 yp23005.51 Homo sapie 1.34e- 13 2 1 4.8 471 184 AA011021 zec9206.51 Scares ret 1.34e- 14 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | •       |             | Match | gt           | n        | ΠD          | escription                  | red. No  |
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| 2 2 5 6 67 111 M.21157                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | •       | 10          |       |              | ıα       | 8410028     | AGNOSTI CHASTAGOS           | 000      |
| 4 22 5.0 472 57 144477 5740 Arabidopsis thal 6.10e- 5 2 5.0 493 55 RICSLS59A Ruce CONA, partial se 6.10e- 5 2 5.0 796 117 W39026 56.010 Human retina CD 6.10e- 8 21 4.8 317 77 CEKK094C2R C-elegans CONA clone 1.34e- 1.8 317 77 CEKK094C2R C-elegans CONA clone 1.34e- 1.8 317 77 CEKK094C2R C-elegans CONA clone 1.34e- 1.8 317 99 N61165 7628703.r1 Homo sapie 1.34e- 1.8 376 199 N61165 752870703.r1 Homo sapie 1.34e- 1.8 376 199 N61165 752870703.r1 Homo sapie 1.34e- 1.8 377 99 N61165 75287004.r1 Homo sapie 1.34e- 1.8 378 57 71079 750004.r1 Homo sapie 1.34e- 1.8 447 184 AA011021 76287001.s1 Homo sapie 1.34e- 1.8 47 184 AA011021 76287001.r1 Homo sapie 1.34e- 1.8 47 184 AA011021 76287001.r1 Homo sapie 1.34e- 1.8 578 137 AA044796 2A67410.r1 Scares ret 1.34e- 1.8 578 137 AA044796 2A67410.r1 Scares ret 1.34e- 1.8 578 137 AA044796 2A67410.r1 Homo sapie 2.59e- 1.8 578 137 AA044796 2A67410.r1 Homo sapie 2.59e- 1.8 578 137 AA06789 2A67400.r1 Homo sapie 2.59e- 1.8 578 137 AA06789 2A67400.r1 Homo sapie 2.59e- 1.8 578 137 AA06789 2A67400.r1 Homo sapie 2.59e- 1.8 578 17177 4.8 A91700.r1 Homo sapie 2.59e- 1.8 578 174 A906789 2A68101.s1 Scares fet 2.59e- 1.8 578 174 A906789 2A68101.s1 Scares fet 2.59e- 1.8 58 177171 4.8 A91710 4.8 A91710 4.8 A91711 8. A91710 4.8 A91711 8. A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A91710 4.8 A9170 6.1 Homo sapie 2.59e- 1.8 50 50 50 50 50 50 50 50 50 50 50 50 50                                                               |         | 10          | •     | o u          | <b>-</b> | 1157        | wayanya. I seracayen        |          |
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| 8 21 4.8 317 7 CELKO94G2R C.elegans CDMA clone 1.34e- 10 4.8 325 19 7 T45404 yb42d03.rl Homo sapie 1.34e- 11 21 4.8 36 166 723370 5c08h02 membrane-free 1.34e- 12 4.8 36 166 723370 5c08h02 membrane-free 1.34e- 13 4.8 37 199 N61165 7628h02 membrane-free 1.34e- 14 8.8 38 47 H45707 yc50c04.rl Homo sapie 1.34e- 15 21 4.8 447 126 R51107 yc50c04.rl Homo sapie 1.34e- 16 21 4.8 447 126 R51107 yc50c04.rl Homo sapie 1.34e- 18 21 4.8 447 126 R51107 yc50c04.rl Homo sapie 1.34e- 19 21 4.8 447 184 AA011021 ze450b06.sl Scares ret 1.34e- 19 21 4.8 447 185 AA021559 ze69b06.sl Scares ret 1.34e- 20 21 4.8 447 186 AA021559 ze69b06.sl Scares ret 1.34e- 21 20 4.6 228 50 R8364 yc12c06.rl Homo sapie 2.59e- 22 20 4.6 278 17 H65650 yc44c09.rl Homo sapie 2.59e- 23 20 4.6 313 2 T60563 yc44c09.rl Homo sapie 2.59e- 24 5.6 349 5 T72764 yc52c03.rl Homo sapie 2.59e- 25 20 4.6 349 5 T72764 yc52c03.rl Homo sapie 2.59e- 26 20 4.6 377 17 AA067387 zd73h08.rl Scares fet 2.59e- 27 4.6 377 17 AA067387 zd73h08.rl Scares fet 2.59e- 28 5 6 4.6 377 17 AA067387 zd73h08.rl Scares fet 2.59e- 39 174 W79653 zd73h08.rl Scares fet 2.59e- 40 4.6 410 17 T48207 yc44c05.rl Homo sapie 2.59e- 41 117 W79653 zd73h08.rl Scares fet 2.59e- 42 42 197 H42207 yc46c06.sl Homo sapie 2.59e- 44 41 165 C20089 xlccccDNA, partial se 2.59e- 44 44 165 C20089 xlccccDNA, partial se 2.59e- 44 44 165 C20089 xlccccDNA, partial se 2.59e- 44 47 186 AA016259 ms49d11.rl Life Tech 2.59e- 44 47 186 AA016259 ms49d11.rl Life Tech 2.59e- 44 47 186 AA016259 ms49d11.rl Life Tech 2.59e- 44 47 186 AA016259 ms49d11.rl Life Tech 2.59e- 44 47 186 AA016259 ms49d11.rl Life Tech 2.59e- 44 47 186 AA016259 ms49d11.rl Life Tech 2.59e- 45 47 47 47 47 47 47 47 47 47 47 47 47 47                                                                                                                                                                                                                                                                                                                                                        |         | . 7         | ٠     | 2            | -        | 56          | 5c10 Human retina c         | 6.10e-0  |
| 9 21 4.8 325 19 T54964 yb42603.Tl Homo sapie 1.34e- 11 4.8 360 166 T23370 Sc08h02 membrane-free 1.34e- 12 4.8 371 99 NG1165 T528h06.rl Pancreatic 1.34e- 13 21 4.8 383 47 H47708 yc50cd4.rl Homo sapie 1.34e- 14 4.8 383 47 H47708 yc50cd4.rl Homo sapie 1.34e- 15 21 4.8 385 5 T71079 yc50cd4.rl Homo sapie 1.34e- 16 21 4.8 447 156 AA011021 Ze69b06.sl Sozes ret 1.34e- 17 4.8 447 156 AA011021 Ze69b06.sl Sozes ret 1.34e- 18 21 4.8 447 156 AA011559 Ze69b06.sl Sozes ret 1.34e- 18 21 4.8 477 156 AA011621 Ze69b06.sl Sozes ret 1.34e- 19 21 20 4.6 228 50 R83564 yc4c09.rl Homo sapie 2.59e- 20 4.6 275 107 H8C2WC112 H. sapiens partial cD 2.59e- 21 20 4.6 373 5 T7177 yc52c03.rl Homo sapie 2.59e- 22 20 4.6 313 7 AA044796 Ze69b06.sl Sozes pre 1.34e- 23 20 4.6 313 7 T7764 yc52c03.rl Homo sapie 2.59e- 24 20 4.6 313 5 T7177 yc52c03.rl Homo sapie 2.59e- 25 20 4.6 314 R828014 yc52c03.rl Homo sapie 2.59e- 26 4.6 37 T777 2 yc52c03.rl Homo sapie 2.59e- 27 20 4.6 37 T777 2 yc52c03.rl Homo sapie 2.59e- 28 20 4.6 37 T777 2 yc52c03.rl Homo sapie 2.59e- 29 20 4.6 37 T777 2 yc52c03.rl Homo sapie 2.59e- 30 4.6 37 T777 2 yc52c03.rl Homo sapie 2.59e- 31 20 4.6 37 T777 2 yc52c03.rl Homo sapie 2.59e- 32 4 5 4 5 7 1177 2 yc52c03.rl Homo sapie 2.59e- 33 2 2 4 5 4 5 7 1177 2 yc74f03.rl Homo sapie 2.59e- 34 2 5 4 5 4 11 17 4 W79538 2d31901.sl Soares fet 2.59e- 35 2 4 6 4 11 17 4 W79538 2d31901.sl Soares fet 2.59e- 36 4 6 4 11 17 4 W79538 2d31901.sl Soares fet 2.59e- 37 7 7 7 4 4 6 4 12 18 AA13652 yc14e06.sl Homo sapie 2.59e- 38 2 2 4 6 4 11 17 Ye820 yc14e06.sl Homo sapie 2.59e- 39 2 4 6 4 11 17 Ye820 yc14e06.sl Homo sapie 2.59e- 30 4 6 4 11 17 Ye820 yc14e06.sl Homo sapie 2.59e- 31 2 4 5 6 7 1 1 1 1 Ye820 yc14e06.sl Homo sapie 2.59e- 32 2 4 6 4 1 1 1 1 Ye820 yc14e06.sl Homo sapie 2.59e- 33 2 2 4 6 6 1 1 1 1 Ye820 yc14e06.sl Homo sapie 2.59e- 34 2 5 7 1 1 1 1 Ye820 yc14e06.sl Homo sapie 2.59e- 35 2 6 7 6 7 6 7 6 7 8 1 1 1 1 1 Ye820 yc14e06.sl Homo sapie 2.59e- 36 7 7 7 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 |         | 7           | •     | -            | 77       | 94GZ        | elegans cDNA clon           | .34e-0   |
| 10 21 4.8 328 168 W40169 5c08D00.rl Pancreatic 1.34e 1.8 360 166 T23370 5c08D02 membrane-free 1.34e 1.8 376 99 NG1165 T9EST292D03.rl Toxop 1.34e 1.8 378 37 171098 Yc50G04.rl Homo sapie 1.34e 1.8 395 5 T71079 Yc50C04.rl Homo sapie 1.34e 1.8 447 184 447 184 7801021 2c69D06.sl Scarces ret 1.34e 1.8 447 184 7801021 2c69D06.sl Scarces ret 1.34e 1.8 447 184 7801021 2c69D06.sl Scarces ret 1.34e 1.8 447 184 7801021 2c69D06.sl Scarces ret 1.34e 1.8 447 184 780806 2c69D06.sl Scarces ret 1.34e 1.8 447 184 780806 2c69D06.sl Scarces ret 1.34e 1.8 447 184 780806 2c69D06.sl Scarces ret 1.34e 1.8 447 184 780806 2c69D06.sl Scarces ret 1.34e 1.8 78 137 780409 2c69D06.sl Scarces ret 1.34e 1.8 78 137 780806 2c69D06.sl Scarces ret 1.34e 1.8 78 137 780806 2c69D06.sl Scarces ret 1.34e 1.34e 1.8 78 137 780806 2c69D06.sl Scarces ret 1.34e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1.36e 1. |         | 7           | •     | ~            | 13       | T54964      | 42d03.rl Homo sapi          | .34e-0   |
| 11 21 4.8 360 166 723370 5508h02 membrane-free 1.34e-1.34e-1.8 371 99 NR1165 TGESTEX27D03.r1 Toxop 1.34e-1.8 383 47 H45707 YC50Gld.r1 Homo sapie 1.34e-1.8 441.26 R53127 YC50Gld.r1 Homo sapie 1.34e-1.8 441.26 R53127 YC50Gld.r1 Homo sapie 1.34e-1.8 441.26 R53127 YC50Gld.r1 Homo sapie 1.34e-1.8 441.26 R53127 YC50Gld.r1 Homo sapie 1.34e-1.8 441.26 R53127 YC50Gld.r1 Homo sapie 1.34e-1.8 441.16 R53127 YC50Gld.r1 Homo sapie 1.34e-1.8 447.156 RA021559 Ze69DG.s1 Scarces ret 1.34e-1.8 451.18 AA09806 Zk67q10.r1 Scarces ret 1.34e-1.8 578 137 AA044796 Zk67q10.r1 Scarces ret 1.34e-1.8 578 137 AA044796 Zk67q10.r1 Scarces ret 1.34e-1.8 578 137 AA09806 Zk67q10.r1 Scarces ret 1.34e-1.8 578 137 AA09806 Zk67q10.r1 Scarces ret 1.34e-1.8 578 137 AA09806 Zk67q10.r1 Homo sapie 2.59e-1.8 578 1717 R6563 Y691C08.r1 Homo sapie 2.59e-1.8 578 1717 R6563 Y691C08.r1 Homo sapie 2.59e-1.8 578 1717 AA067387 Zc12d10.s1 Scarces fet 2.59e-1.8 578 1717 AA067387 Zc12d10.s1 Scarces fet 2.59e-1.8 578 1717 AA067387 Zc12d10.s1 Scarces fet 2.59e-1.8 578 1717 AA067387 Zc12d10.s1 Scarces fet 2.59e-1.8 578 1717 AA067387 Zc12d10.s1 Scarces fet 2.59e-1.8 578 1717 AA067387 Zc12d10.s1 Scarces fet 2.59e-1.8 578 1717 AA067387 Zc12d10.s1 Scarces fet 2.59e-1.8 578 1717 AA067387 Zc12d10.s1 Scarces fet 2.59e-1.8 58 1717 Tc12d10.s1 Scarces fet 2.59e-1.8 58 1718 Tc12d10.s1 Scarces fet 2.59e-1.8 58 1718 Tc12d10.s1 Scarces fet 2.59e-1.8 58 1718 Tc12d10.s1 Scarces fet 2.59e-1.8 58 1718 Tc12d10.s1 Scarces fet 2.59e-1.8 58 1718 Tc12d10.s1 Scarces fet 2 | Ã       | ~           |       | N            | ø        | 9           | 282h06 rl Pancreati         | 1.346-   |
| 12 21 4.8 371 99 Noili65 TGESTEXTZTD03.r1 Toxop 1.34e-134e-134e-134e-134e-134e-134e-134e-1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |         | 2           |       | ·            | · ·      | -           | OShO2 membrane-fre          | 346      |
| 13   21   4.8   376   5   71708   9750044.71   Homo sapie   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34e-1   1.34   | -       | 2           |       | -            | 000      | · K         | 5ST2 V 27 PO 3 T 1 TO 4 O D | 346-0    |
| 15 21 4.8 38.4 7 H4570 7 YP23105.51 Homo sapie 1.34e-1.6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | -       |             | •     | ٠,           | ď        | 1111000     | CACA THOMOSTAL TOWN         | 0 7 7    |
| 15 21 4.8 395 7 171079 YC50c04.71 Homo sapie 1.34e-14.8 44126 R53127 Y96605.71 Homo sapie 1.34e-14.8 447.184 447.185 AA011021 Ze69D06.51 Soarces ret 1.34e-18.8 447.184 447.185 AA011021 Ze69D06.51 Soarces ret 1.34e-19.8 447.184 447.185 AA019806 Ze69D06.51 Soarces ret 1.34e-19.8 447.184 447.184 AA011021 Ze69D06.51 Soarces ret 1.34e-19.8 4.8 471.8 AA044796 Ze69D06.51 Soarces pre 1.34e-19.8 578 137 AA048806 Ze67G10.71 Homo sapie 2.59e-20.4 6.27 107 HSC2WC112 H Capiens partial CD 2.59e-20.4 6.27 107 HSC2WC112 H Capiens partial CD 2.59e-20.4 6.3 31 2 T6053 Y691C08.71 Homo sapie 2.59e-20.4 6.3 49 11 H83210 Y691C08.71 Homo sapie 2.59e-20.4 6.3 40 57 1717 4 M79538 Ze623.1 Homo sapie 2.59e-30.4 6.3 77 174 AM067387 Ze623.1 Homo sapie 2.59e-30.4 6.4 411 174 A4827 Y65 Sall Olive Sapie 2.59e-30.4 6.4 411 174 A4827 Y65 Ze61 Homo sapie 2.59e-30.4 6.4 411 174 A4827 Y65 Ze61 Homo sapie 2.59e-30.4 6.4 429 53 R92022 Y96606.5.1 Homo sapie 2.59e-40.6 429 53 R92022 Y96606.5.1 Homo sapie 2.59e-40.6 429 53 R92022 Y96606.5.1 Homo sapie 2.59e-40.6 420 75 H97934 Yw6604.5.1 Homo sapie 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 Lambda-PRL2 Ara 2.59e-40.6 420 75 H97934 Ze623 La | - 1     | 40          | ٠     | - α          | , [      | 171000      | 32hOF 51 HOWO SAPI          | 0.046    |
| 15 21 4.8 44126 R3317 YG96a05.11 Homo saple 1.34e-114.8 447184 AA011021 2e34c01.51 Scarces ret 1.34e-118.8 447184 AA011021 2e34c01.51 Scarces ret 1.34e-118.8 AA028806 2x44d06.51 Stratagene 1.34e-118.8 AA028806 2x44d06.51 Stratagene 1.34e-119.2 4.6 278 137 AA044796 2x67q10.71 Scarces pre 1.34e-119.2 4.6 278 137 AA044796 2x67q10.71 Homo saple 2.59e-119.8 20 4.6 275 107 HSC2WC112 H. Saplens partial cD 2.59e-119.8 20 4.6 375 107 HSC2WC112 H. Saplens partial cD 2.59e-119.8 20 4.6 375 107 HSC2WC112 H. Saplens partial cD 2.59e-119.8 20 4.6 349 5 772764 YC51al0.71 Homo saple 2.59e-119.8 20 4.6 349 5 772764 YC51al0.71 Homo saple 2.59e-119.8 20 4.6 370 77 772764 YC51al0.71 Homo saple 2.59e-119.8 20 4.6 370 77 772764 YC51al0.71 Homo saple 2.59e-119.8 20 4.6 370 77 77276 YC51al0.71 Homo saple 2.59e-119.8 20 4.6 370 77 77276 YC51al0.71 Homo saple 2.59e-119.8 20 4.6 411 77 748207 YC51al0.71 Homo saple 2.59e-119.8 20 4.6 411 77 748207 YC51al0.71 Homo saple 2.59e-119.8 20 4.6 420 75 H97994 YW18009.51 Scarces fet 2.59e-119.8 20 4.6 420 75 H97994 YW18009.51 Scarces fet 2.59e-119.8 20 4.6 420 75 H97994 YW18009.51 Scarces fet 2.59e-119.8 20 4.6 420 75 H97994 YW18009.51 Scarces fet 2.59e-119.8 20 4.6 420 75 H97994 YW06e04.51 Homo saple 2.59e-119.8 20 4.6 420 75 H97994 YW18009.51 Scarces fet 2.59e-119.8 20 4.6 420 75 H97994 YW18009.51 Scarces fet 2.59e-119.8 20 4.6 420 75 H97994 YW18009.51 Scarces fet 2.59e-119.8 20 4.6 420 75 H97994 YW18009.51 Scarces fet 2.59e-119.8 20 4.6 420 75 H97994 YW18009.51 Scarces fet 2.59e-119.8 20 4.6 441 165 C20089 Rice CDNA, partial se 2.59e-119.8 20 4.6 441 165 C20089 Rice CDNA, partial se 2.59e-119.8 20 4.6 441 165 C20089 Rice CDNA, partial se 2.59e-119.8 20 4.6 441 165 C20089 YW18009.51 Homo saple 2.59e-119.8 20 4.6 441 165 C20089 YW18009.51 Homo saple 2.59e-119.8 20 4.6 441 165 C20089 YW18009.51 Homo saple 2.59e-119.8 20 4.6 441 165 C20089 YW18009.51 Homo saple 2.59e-119.8 20 4.6 441 165 C20089 YW18009.51 Homo saple 2.59e-119.8 20 4.6 441 165 C20089 YW18009.51 Homo saple 2.59e-119.8 20 4.6 441 165  | - 1     |             |       | 0            | - u      | 070         | SOLO SEL HOMO SELL          | 0 0 0    |
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| 17                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 1 .     | 4 (         |       | * *          | 0 0      | - 0         | seaus.ri Homo sapi          | .34e-04  |
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| 22 20 4.6 271 4 T69650 yc44C09.rl Homo sapie 2.59e-23 2 4.6 275 107 H8C2WC112 H. Sapiens Partial CD 2.59e-25 2 4.6 323 2 T71717 H Sapiens Partial CD 2.59e-25 2 4.6 331 2 T60563 yc951C08.rl Homo sapie 2.59e-26 2.0 4.6 369 T H83210 yc951C08.rl Homo sapie 2.59e-27 2 4.6 369 T H83210 yc975f02.sl Homo sapie 2.59e-29 2 4.6 374 78 R88014 yc75f02.sl Homo sapie 2.59e-37 146 377 T74 AA067387 26232 Lambda-PRL2 Ara 2.59e-37 146 411 T7 44827 2 26232 Lambda-PRL2 Ara 2.59e-37 146 411 T7 44827 2 26232 Lambda-PRL2 Ara 2.59e-37 146 411 T7 44827 2 26232 Lambda-PRL2 Ara 2.59e-37 146 411 T7 44827 2 2124d10.sl Soares fet 2.59e-37 146 420 75 H9338 2481901.sl Soares fet 2.59e-38 2 4.6 420 75 H9339 20 4.6 420 75 H9331 2 20 4.6 420 75 H9339 2 2124d10.sl Soares fet 2.59e-38 2 4.6 420 75 H9339 2 2124d10.sl Soares fet 2.59e-40 4.6 420 75 H97994 yw06e04.sl Homo sapie 2.59e-40 4.6 441 165 C20089 Rice CDNA, partial se 2.59e-41 2 2 4.6 441 165 C20089 Rice CDNA, partial se 2.59e-41 2 2 4.6 453 74 H93043 yag4431.rl Life Tech 2.59e-42 2 4.6 442 75 8 H99043 yag44303.rl Homo sapie 2.59e-42 2 4.6 453 74 H93043 yag44303.rl Homo sapie 2.59e-42 2 4.6 451 74 H93043 yag44303.rl Homo sapie 2.59e-42 2 4.6 472 83 H90943 yag44303.rl Homo sapie 2.59e-42 2 4.6 472 83 H90943 yag44303.rl Homo sapie 2.59e-42 2 4.6 472 83 H90943 yag44303.rl Homo sapie 2.59e-42 2 4.6 472 83 H90943 yag44303.rl Homo sapie 2.59e-42 2 4.6 472 83 H90943 yag44303.rl Homo sapie 2.59e-42 2 4.6 472 83 H90943 yag44303.rl Homo sapie 2.59e-42 3 4.6 614 10 N63920 yag463.rl Homo sapie 2.59e-42 3 4.6 472 83 H90943 yag44303.rl Homo sapie 2.59e-42 3 4.6 614 10 N63920 yag463.rl Homo sapie 2.59e-42 3 4.6 614 14 14 14 14 14 14 14 14 14 14 14 14 1                                                                                                                                                                                                                                                                                                                                                                           | ď       | C)          | ٠     | 2            | 20       | R83564      | 12e06.rl Homo sapi          | .59e-0   |
| 23 20 4.6 275 107 HSC2WC112 H. sapiens partial cD 2.59e 24 6.6 31.9 5 T0563 9.9 10.0 11.0 v552c03.rl Homo sapie 2.59e 25 4.6 31.9 5 T0563 9.9 10.0 rl Homo sapie 2.59e 25 20 4.6 314 5 T2764 yc51a10.rl Homo sapie 2.59e 28 20 4.6 374 18 H83210 yq47d03.rl Homo sapie 2.59e 29 20 4.6 375 146 W06794 SMESTO430 SCHIStCOSMA 2.59e 30 20 4.6 377 177 AA067387 26232 Lambda-PRL2 Ara 2.59e 31 20 4.6 411 17 44827 26332 Lambda-PRL2 Ara 2.59e 32 20 4.6 411 17 74827 26332 Lambda-PRL2 Ara 2.59e 33 20 4.6 411 17 74827 26480 1.5 Soarces fet 2.59e 35 20 4.6 420 197 H94319 yv18b09.sl Soarces fet 2.59e 35 20 4.6 420 197 H94319 yv18b09.sl Soarces fet 2.59e 36 20 4.6 420 57 H94319 yv18b09.sl Soarces fet 2.59e 36 20 4.6 420 197 H94319 yv18b09.sl Soarces fet 2.59e 420 4.6 420 420 420 420 420 420 420 420 420 420                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 7       | 7           | ٠     | 7            | 4        | T69650      | 14c09.rl Homo sapi          | .59e-0   |
| 24 20 4.6 323 5 T71171 yc52c03.rl Homo sapie 2.59e- 25 20 4.6 349 2 T72663 yb91c08.rl Homo sapie 2.59e- 26 20 4.6 349 7 T80563 yb91c08.rl Homo sapie 2.59e- 27 20 4.6 349 71 H83210 yq47d03.rl Homo sapie 2.59e- 28 20 4.6 374 78 R808014 yq476d3.rl Homo sapie 2.59e- 29 20 4.6 377 177 AA067387 26232 Lambda-PRL2 Ara 2.59e- 30 20 4.6 377 177 AA067387 26232 Lambda-PRL2 Ara 2.59e- 31 20 4.6 411 17 T48207 yb44a06.sl Homo sapie 2.59e- 33 20 4.6 411 17 T48207 yb44a06.sl Homo sapie 2.59e- 34 20 4.6 420 197 H94319 yv18b09.sl Soares fet 2.59e- 35 20 4.6 420 75 H97994 yw06e04.sl Homo sapie 2.59e- 36 20 4.6 429 75 H97994 yw06e04.sl Homo sapie 2.59e- 37 20 4.6 429 75 H97994 yw06e04.sl Homo sapie 2.59e- 38 20 4.6 429 75 H97994 yw06e04.sl Homo sapie 2.59e- 40 4.6 441 165 C20089 Rice cDNA, partial se 2.59e- 41 20 4.6 453 104 N4309 yv06h02.sl Homo sapie 2.59e- 42 20 4.6 453 104 N4309 yv06h02.sl Homo sapie 2.59e- 44 45 74 H33069 yv06h02.sl Homo sapie 2.59e- 45 46 472 83 H80943 yy848031.rl Life Tech 2.59e- 46 472 83 AA166259 ms49d11.rl Life Tech 2.59e- 47 20 4.6 641 10 N63920 yv06h02.sl Homo sapie 2.59e- 48 20 4.6 472 83 H80943 yy848031.rl Homo sapie 2.59e- 49 20 4.6 472 83 H80943 yy848031.rl Life Tech 2.59e- 40 4.6 472 83 H80943 yy848031.rl Life Tech 2.59e- 41 20 4.6 641 18 AN166259 ms49d11.rl Life Tech 2.59e- 42 20 4.6 641 18 AN166259 ms49d11.rl Life Tech 2.59e- 43 20 4.6 641 18 AN166259 ms49d11.rl Life Tech 2.59e- 44 20 4.6 641 18 AN166259 ms49d11.rl Life Tech 2.59e- 45 472 83 H80943 yy84803.rl Homo sapie 2.59e- 46 472 83 H80943 yy84803.rl Homo sapie 2.59e- 47 57 64 57 74 H3004 yy8403.rl Homo sapie 2.59e- 48 57 64 57 74 H3004 yy8403.rl Homo sapie 2.59e- 49 50 40 60 193 AN166259 yy86031.rl Life Tech 2.59e- 40 50 40 60 193 AN166259 yy86031.rl Life Tech 2.59e- 40 50 40 60 193 AN166259 yy86031.rl Life Tech 2.59e- 40 50 50 50 50 50 50 50 50 50 50 50 50 50                                                                                                                                                                                          | 7       | 7           | ٠     | 7            | Ö        | WC11        | sapiens partial c           | 2.59e-   |
| 25 20 4.6 331 2 T60563 yb91c08.rl Homo sapie 2.59e- 26 2.6 4.6 369 5 T72764 yc51al0.rl Homo sapie 2.59e- 27 2.0 4.6 369 TH 883210 yq47d03.rl Homo sapie 2.59e- 28 2.0 4.6 374 78 R88014 yq75f02.sl Homo sapie 2.59e- 29 2.0 4.6 377 TA AA067387 26232 Lambda-PRL2 Ara 2.59e- 31 2.0 4.6 377 TA AA067387 26232 Lambda-PRL2 Ara 2.59e- 32 2.0 4.6 411 TA 448207 yb44a06.rl Soares fet 2.59e- 33 2.0 4.6 412 185 AA135635 z124d10.sl Soares fet 2.59e- 34 2.0 4.6 420 75 H97934 yw06e04.sl Homo sapie 2.59e- 35 2.0 4.6 420 75 H97934 yw06e05.sl Homo sapie 2.59e- 36 2.0 4.6 429 53 R92022 yp96e05.sl Homo sapie 2.59e- 37 2.0 4.6 441 165 C20089 Rice cDNA, partial se 2.59e- 40 4.6 441 165 C20089 Rice cDNA, partial se 2.59e- 41 2.0 4.6 453 104 H97439 yw06h02.sl Homo sapie 2.59e- 42 2.0 4.6 441 165 C20089 Rice cDNA, partial se 2.59e- 43 2.0 4.6 453 104 H97439 yw06h02.sl Homo sapie 2.59e- 44 45 47 48 H97439 yw06h02.sl Homo sapie 2.59e- 45 46 472 81 H90943 yw06h02.sl Homo sapie 2.59e- 46 472 83 H09043 yw06h02.sl Homo sapie 2.59e- 47 20 4.6 472 83 H09043 yw06h02.sl Homo sapie 2.59e- 48 20 4.6 472 83 H09043 yw06h02.sl Homo sapie 2.59e- 48 20 4.6 472 83 H09043 yw06h02.sl Homo sapie 2.59e- 49 20 4.6 472 83 H09043 yw06h02.sl Homo sapie 2.59e- 41 20 4.6 472 83 H09043 yw06h02.sl Homo sapie 2.59e- 42 20 4.6 472 83 H09043 yw06h02.sl Homo sapie 2.59e- 43 20 4.6 472 83 H09043 yw06h02.sl Homo sapie 2.59e- 44 20 4.6 472 83 H09043 yw06h02.sl Homo sapie 2.59e- 45 20 4.6 472 83 H09043 yw06h02.sl Homo sapie 2.59e- 47 20 4.6 472 83 H09043 yw06h02.sl Homo sapie 2.59e- 48 20 4.6 6141 10 N63920 yw06h02.sl Homo sapie 2.59e-                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Ŕ       | 7           | ٠     | 2            | S        | T71171      | 203.rl Homo sapi            | .59e-0   |
| 26 20 4.6 349 5 T72764 yc51al0.rl Homo sapie 2.59e- 27 20 4.6 369 71 H82210 yq47403.rl Homo sapie 2.59e- 28 20 4.6 374 78 R8810 yq476403.rl Homo sapie 2.59e- 29 20 4.6 375 146 W06794 SMEST0430 Schistcosoma 2.59e- 30 20 4.6 377 177 AA067387 26232 Lambda-PRL2 Ars 2.59e- 31 20 4.6 410 174 W79538 2d31901.sl Soares fet 2.59e- 32 20 4.6 411 17 T48207 yb4806.sl Homo sapie 2.59e- 34 20 4.6 412 185 AA135635 2124010.sl Soares fet 2.59e- 35 20 4.6 420 37 H94319 yv08606.sl Homo sapie 2.59e- 36 20 4.6 429 75 H94319 yv08609.sl Soares fet 2.59e- 37 20 4.6 429 75 H94319 yv1809.sl Soares fet 2.59e- 38 20 4.6 429 75 H94319 yv1809.sl Soares fet 2.59e- 39 20 4.6 429 75 H94319 yv1809.sl Soares fet 2.59e- 40 4.6 425 68 H72171 yv99606.sl Homo sapie 2.59e- 41 20 4.6 443 68 H72171 yr99906.rl Homo sapie 2.59e- 42 20 4.6 453 104 M74503 za5403.sl Homo sapie 2.59e- 43 20 4.6 451 14 H33069 yv06h02.sl Homo sapie 2.59e- 44 20 4.6 450 193 AA166259 ms49d11.rl Life Tech 2.59e- 45 20 4.6 472 83 AA166259 ms49d11.rl Life Tech 2.59e- 46 472 83 AA166259 ms49d11.rl Life Tech 2.59e- 47 20 4.6 614 10 N63920 yv06h02.sl Homo sapie 2.59e- 48 20 4.6 614 10 N63920 yv06h02.sl Homo sapie 2.59e- 48 20 4.6 457 83 AA166259 ms49d11.rl Life Tech 2.59e- 49 20 4.6 614 10 N63920 yv06h02.sl Homo sapie 2.59e- 40 4.6 472 83 AA166259 ms49d11.rl Life Tech 2.59e- 41 20 4.6 614 10 N63920 yv06h02.sl Homo sapie 2.59e- 42 20 4.6 614 10 N63969 zapie 2.59e- 43 20 4.6 614 10 N63969 zapie 2.59e- 44 20 4.6 457 34 H33069 zapie 2.59e- 45 20 4.6 614 10 N63969 zapie 2.59e- 46 472 83 AA166259 zapie 2.59e- 475 472 83 AA166259 zapie 2.59e- 48 20 4.6 614 10 N63969 zapie 2.59e-                                                                                                                                                                                                                                                                                                                                                                                                                                       | ₹       | ~           | ٠     | 3            | 7        | T60563      | :08.rl Homo sapi            | .59e-0   |
| 27 20 4.6 369 71 H83210 7947dd3.rl Homo sapie 2.59e-28e-28e-28e-28e-28e-28e-28e-28e-28e-28                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ñ       | 7           | ٠     | 4            | Ŋ        | T72764      | alo.rl Homo sapi            | .59e-0   |
| 28 20 4.6 874 78 R88014 9q75f02.sl Homo sapie 2.59e- 29 20 4.6 375 146 M06794 SMEST0430 SCHISLCOOM 2.59e- 30 20 4.6 377 177 AA067387 2d73h08.rl Scarcs fet 2.59e- 31 20 4.6 411 174 M79538 2d73h08.rl Scarcs fet 2.59e- 32 20 4.6 411 174 M79538 2d73h08.rl Scarcs fet 2.59e- 33 20 4.6 411 177 M48207 YA4406.sl Homo sapie 2.59e- 35 20 4.6 420 75 H97994 YA06604.sl Homo sapie 2.59e- 36 20 4.6 429 53 R92022 YP96e05.sl Homo sapie 2.59e- 37 20 4.6 429 53 R92022 YP96e05.sl Homo sapie 2.59e- 38 20 4.6 429 53 R92022 YP96e05.sl Homo sapie 2.59e- 40 40 40 40 40 40 40 40 40 40 40 40 40 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | .7      | 7           | ٠     | 9            | 71       | H83210      | 103.rl Homo sapi            | .59e-0   |
| 29 20 4.6 375 146 W06794 SMEST0430 Schistosoma 2.59e 30 4.6 377 177 A4067387 26232 Lambda-PRLZ 5.59e 31 20 4.6 390 174 W79538 2d73108 r.l Soares fet 2.59e 32 2d. 4.6 411 174 W79538 2d31001.s1 Soares fet 2.59e 34 4.6 412 185 A413595 2124d10.s1 Soares fet 2.59e 35 20 4.6 420 197 H94319 yv18b09.s1 Soares fet 2.59e 35 20 4.6 420 197 H94319 yv18b09.s1 Soares fet 2.59e 36 20 4.6 429 75 H97994 yv08b09.s1 Soares fet 2.59e 37 H07994 yv08b09.s1 Soares fet 2.59e 37 H07994 yv08b09.s1 Soares fet 2.59e 37 H07994 yv08b09.s1 H070 sapie 2.59e 38 20 4.6 429 53 R2022 yp96605.s1 H070 sapie 2.59e 40 41 165 C20472 Rice cDNA, partial se 2.59e 41 165 C20472 Rice cDNA, partial se 2.59e 41 165 C2089 yv06h02.s1 H070 sapie 2.59e 41 165 C2089 yv06h02.s1 H070 sapie 2.59e 41 165 C2089 yv06h02.s1 H070 sapie 2.59e 41 165 C2089 yv06h02.s1 H070 sapie 2.59e 41 167 472 38 H03043 yv06h02.s1 H070 sapie 2.59e 41 167 10 10 10 10 10 10 10 10 10 10 10 10 10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 7       | 7           |       | ~            | 78       | R98014      | f02.sl Homo sapi            | .59e-0   |
| 30 20 4.6 377 177 AA067387 26222 Lambda-PRL2 Ara 2.59e 31 20 4.6 390 174 W79653 2d3108.rt Soares fet 2.59e 33 20 4.6 411 17 W79538 2d3108.rt Soares fet 2.59e 32 20 4.6 411 17 T48207 yb44a06.s1 Home sapie 2.59e 35 20 4.6 420 189 H94319 yv18b09.s1 Soares pre 2.59e 36 20 4.6 420 197 H94319 yv06e04.s1 Home sapie 2.59e 37 20 4.6 429 75 H97994 yv06e04.s1 Home sapie 2.59e 38 20 4.6 429 58 R2202 yp96e05.s1 Home sapie 2.59e 40 40 41 165 C20472 Rice cDNA, partial se 2.59e 41 165 C20472 Rice cDNA, partial se 2.59e 41 105 C20489 Rice cDNA, partial se 2.59e 42 104 W44 165 C20489 Rice cDNA, partial se 2.59e 42 104 W44 165 C20489 Rice cDNA, partial se 2.59e 42 104 W44 165 C2089 Rice cDNA, partial se 2.59e 42 104 W44 165 C2089 Rice cDNA, partial se 2.59e 42 104 W44 105 C2089 Rice cDNA, partial se 2.59e 42 104 W44 105 C2089 Rice cDNA, partial se 2.59e 42 104 W44 105 C2089 Rice cDNA, partial se 2.59e 42 104 W44 105 C2089 Rice CDNA, partial se 2.59e 44 105 C2089 Rice CDNA, partial se 2.59e 45 104 H93069 V06h02.s1 Home sapie 2.59e 45 104 H0048 Sapie 2.59e W45 104 W64 105 M849431.rt Home sapie 2.59e W64 105 M849431.rt Home sapie 2.59e W64 105 M849431.rt Home sapie 2.59e W64 105 M849431.rt Home sapie 2.59e W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W64 105 W6 | 7       | 7           | ٠     | ^            | 4        | 94          | ST0430 Schistosom           | .59e-0   |
| 31 20 4.6 411 74 W79553 2d73h08.r1 Soares fet 2.59e 2d 4.6 411 17 748207 2d81901.s1 Soares fet 2.59e 31 20 4.6 411 17 748207 2d81901.s1 Soares fet 2.59e 32 4.6 411 17 748207 2d81901.s1 Soares pre 2.59e 35 20 4.6 412 185 AA135635 214d10.s1 Soares pre 2.59e 36 20 4.6 420 75 H9939                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ์<br>พี | 7           | ٠     | 7            | 7        | 738         | 32 Lambda-PRL2 A            | 2.59e    |
| 32 20 4.6 411174 W79538 2d81901.s1 Soares fet 2.59e 3.8 2d 4.6 411 17 T48207 yb44a06.s1 Homo saple 2.59e 3.4 20 4.6 412 197 H94319 yv18b09.s1 Soares pre 2.59e 3.5 20 4.6 420 197 H94319 yv18b09.s1 Soares fet 2.59e 3.6 20 4.6 429 53 H97994 yw06e04.s1 Homo saple 2.59e 3.7 20 4.6 429 53 H97994 yw06e04.s1 Homo saple 2.59e 3.8 20 4.6 429 53 H97202 yp96e05.s1 Homo saple 2.59e 4.0 4.6 435 68 H72171 yr99906.r1 Homo saple 2.59e 4.0 4.6 441 165 C20472 Rice CDNA, partial se 2.59e 4.1 20 4.6 453 104 N74503 za54h03.s1 Homo saple 2.59e 4.2 20 4.6 457 44 H33069 yv06h02.s1 Homo saple 2.59e 4.5 4.6 472 83 H50943 ms49d11.r1 Life Tech 2.59e 4.5 6.4 6.1 1 N63943 yp84e03.r1 Homo saple 2.59e 4.5 6.4 10 N63920 za28h09.s1 Homo saple 2.59e 4.5 6.4 10 N63920 za28h03.s1 Homo saple 2.59e 4.5 6.4 10 N63920 za28h03.s1 Homo saple 2.59e 4.5 6.4 10 N63920 za28h03.s1 Homo saple 2.59e 4.5 6.4 10 N63920 za28h03.s1 Homo saple 2.59e 4.5 6.4 10 N63920 za28h03.s1 Homo saple 2.59e 4.5 6.4 10 N63920 za28h03.s1 Homo saple 2.59e 4.5 6.4 10 N63920 za28h03.s1 Homo saple 2.59e 4.5 6.4 10 N63920 za28h03.s1 Homo saple 2.59e                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | m       | 7           | ٠     | g            | /        | Ś           | 3h08.rl Soares f            | 2.59e-0  |
| 33 20 4.6 41117 T48207 yb44a06.s1 Homo sapie 2.59e-34 20 4.6 412 185 AA135635 Z124d10.s1 Soarces pre 2.59e-35 20 4.6 420 197 H94319 yv08b09.s1 Soarces pre 2.59e-36 20 4.6 429 75 H97994 yw06e04.s1 Homo sapie 2.59e-38 20 4.6 429 53 R2202 y996e05.s1 Homo sapie 2.59e-39 20 4.6 435 68 H72171 yr99906.r1 Homo sapie 2.59e-40 20 4.6 441 165 C20472 Rice CDNA, partial se 2.59e-41 20 4.6 453 104 N74503 Za5403.s1 Homo sapie 2.59e-42 20 4.6 457 74 H33069 yv06h02.s1 Homo sapie 2.59e-43 20 4.6 450 193 AA166259 ms49d11.r1 Life Tech 2.59e-44 20 4.6 472 83 H83043 yp848403.r1 Homo sapie 2.59e-45 20 4.6 472 83 H80943 yp848403.r1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-54 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 10 N63920 za28h09.s1 Homo sapie 2.59e-45 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 4.6 614 20 | m       | ~           |       | -            | _        | m           | lg01.sl Soares f            | 2.59e-0  |
| 34 20 4.6 420 197 H94319 yv18b09.s1 Soares pre 2.59e 35 20 4.6 420 197 H94319 yv18b09.s1 Soares fet 2.59e 36 20 4.6 429 53 H97994 yw06e04.s1 Homo sapie 2.59e 37 20 4.6 429 53 R92022 yp96e05.s1 Homo sapie 2.59e 4.6 441 165 C20472 Rice CDNA, partial se 2.59e 4.6 441 165 C2049 Rice CDNA, partial se 2.59e 4.6 444 165 C2049 Rice CDNA, partial se 2.59e 4.6 4.6 4.8 4.9 30 8 Rice CDNA, partial se 2.59e 4.6 4.5 74 H93069 yv06h02.s1 Homo sapie 2.59e 4.6 4.5 74 H93069 yv06h02.s1 Homo sapie 2.59e 4.6 4.5 4.8 4.8 30 8 Ms49d11.r1 Life Tech 2.59e 4.5 4.6 4.1 10 N63920 RSAPON STANDAR SAPIR S.59e 4.5 6.14 10 N63920 RSAPON STANDAR SAPIR S.59e 4.5 6.14 10 N63920 RSAPON STANDAR SAPIR S.59e 4.5 6.14 10 N63920 RSAPON STANDAR SAPIR S.59e 4.5 6.14 10 N63920 RSAPON STANDAR SAPIR S.59e 4.5 6.14 10 N63920 RSAPON STANDAR SAPIR S.59e 4.5 6.14 10 N63920 RSAPON STANDAR SAPIR S.59e 4.5 6.14 10 N63920 RSAPON STANDAR SAPIR S.59e 4.5 6.14 10 N63920 RSAPON STANDAR SAPIR S.59e 4.5 6.14 10 N63920 RSAPON STANDAR SAPON SAPON STANDAR SAPON STANDAR SAPON STANDAR SAPON SAPON STANDAR SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON SAPON S | m       | 7           | ٠     | -1           | 7        | T48207      | 106.sl Homo sapi            | 2.59e-0  |
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| 36 20 4.6 429 75 H97994 yw06e04.s1 Homo sapie 2.59e-37 20 4.6 429 53 R92022 yp96e05.s1 Homo sapie 2.59e-38 20 4.6 435 68 H72171 yr99g06.r1 Homo sapie 2.59e-40 20 4.6 441 165 C20472 Rice CDNA, partial se 2.59e-41 20 4.6 453 104 N74503 za54h03.s1 Homo sapie 2.59e-42 20 4.6 457 74 H33069 yv06h02.s1 Homo sapie 2.59e-43 20 4.6 472 83 H09943 yp84403.r1 Homo sapie 2.59e-44 20 4.6 647 83 H09943 yp84403.r1 Homo sapie 2.59e-45 20 4.6 647 81 H09943 yp84403.r1 Homo sapie 2.59e-45 20 4.6 647 81 N0943 yp84403.r1 Homo sapie 2.59e-45 20 4.6 647 81 N0943 yp84403.r1 Homo sapie 2.59e-45 20 4.6 647 81 N0943 yp84403.r1 Homo sapie 2.59e-45 20 4.6 647 81 N0943 yp84403.r1 Homo sapie 2.59e-759e-759e-759e-759e-759e-759e-759e-7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | m       | 7           | ٠     | N            | g        | Н           | 3b09.sl Soares f            | 2.59e-   |
| 37 20 4.6 429 53 R92022                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | m       | 7           | ٠     | ~            | 75       | H97994      | 904.sl Homo sapi            | 2.59e-0  |
| 38 20 4.6 435 68 H72171                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | m       | 7           | ٠.    | N            | 23       | R92022      | 05.sl Homo sapi             | 596-0    |
| 39 20 4.6 441 165 C20472 Rice cDNA, partial se 2.59e 40 20 4.6 444 165 C20089 Rice cDNA, partial se 2.59e 41 20 4.6 453 104 N74503 za54h03.s1 Homo sapie 2.59e 42 20 4.6 457 44 H33069 yv06h02.s1 Homo sapie 2.59e 43 20 4.6 470 193 AA166259 ms49d11.r1 Life Tech 2.59e 44 20 4.6 472 83 H50943 ypg4403.r1 Homo sapie 2.59e 45 614 101 N63920 za28h09 s1 Homo sapie 2.59e 45 614 101 N63920                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ñ       | 7           | -     | m            | 68       | H72171      | 3006.rl Homo sapi           | 596-0    |
| 40 20 4.6 444 165 C20089 Rice CDNA, partial se 2.59e 41 20 4.6 453 104 N74503 za54h03.51 Homo sapie 2.59e 42 20 4.6 457 74 H93069 yv06h02.51 Homo sapie 2.59e 43 20 4.6 460 193 AA166259 ms49d11.r1 Life Tech 2.59e 44 20 4.6 472 83 H90943 ypg48403.r1 Homo sapie 2.59e 45 614 101 N63920 za28h09 s1 Homo sapie 2.59e 45 614 101 N63920                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ń       | 2           | ٠.    | 4            | 9        | 7           | se cDNA, partial s          | 2.59e-0  |
| 41 20 . 4.6 453 104 N74503 za54h03.s1 Homo sapie 2.59e 42 20 4.6 457 74 H93069 yv06h02.s1 Homo sapie 2.59e 43 20 4.6 460 193 AA166259 ms49d11.r1 Life Tech 2.59e 44 20 4.6 472 83 H50943 yp84a03.r1 Homo sapie 2.59e 45 614 101 N63420 za28h04 s1 Homo sapie 2.59e 5 59e 514 101 N63420                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 4       | 7           | -     | 4            | 9        | ω           | se cDNA, partial s          | -59e-    |
| 42 20 4.6 457 74 H93069 yv06h02.sl Homo saple 2.59e-43 20 4.6 450 193 AA166259 ms4d311.rl Life Tech 2.59e-44 20 4.6 472 83 H50943 yp84d03.rl Homo saple 2.59e-45 20 4.6 614 101 N63420                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 4       | 7           | -     | S            | Ò        | 0           | 14h03.sl Homo sapi          | .59e-0   |
| 43 20 4.6 460 193 AA166259 ms49d11.rl Life Tech 2.59e<br>44 20 4.6 472 83 H50943 yp84403.rl Homo sapile 2.59e-<br>45 20 4.6 614 101 N63920 za28ANG sl Home sapile 2.59e-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 4       | 7           | ٠.    | 'n           | 74       | H93069      | Sh02.sl Homo saple          | .59e-03  |
| 44 20 4.6 472 83 H50943 yp84a03.rl Homo sapie 2.59e-45 20 4.6 614 101 N63920 za28h09 sl Homo sapie 2.59e-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 4       | 7           | -     | Θ            | σ        | 625         | 849dll rl Life Tec          | 2 59p-   |
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## ALIGNMENTS

mrna EST 10-JUL-1995 ym62a05.r1 Homo sapiens cDNA clone 163472 5' similar to SP:S32367 832367 ALPA-SNAP PROTEIN - i. DEFINITION ACCESSION NID KEYWORDS

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/organism="Homo sapiens"
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300 bp mRNA EST 28-OCT-1996 550527 5'. Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone AA100384
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1 (bases 1 to 344)
11 lier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohling, T., Soares, M., Tan, F., Materston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
High quality sequence stops: 313
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Tel: 314 286 1800
Fax: 314 286 1810
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WashU-Merck EST Project
Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson, R.
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     SOURCE
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopterayil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Butheria; Archorta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 453)
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Location/Qualifiers
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Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Wash U-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N21157 453 bp mRNA EST 19-DEC yx47d01.s1 Homo sapiens cDNA clone 264865 3' similar to SP:TCPB_MOUSE P80314 T-COMPLEX PROTEIN 1, BETA SUBUNIT ;
                                                                                                                                                                                                                                                                Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 GIACCTICATIATGACGAAGAACCTCTCATCAGCTGTTGTGTGACAAATGT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 183; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 15; Indels
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/lab_host="SOLR (kanamycin resistant)"
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Pred. No. 6.10e-06;
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27-JUL-1995

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EST(expressed sequence tag). Oryza sativa (8 days old) cDNA to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens

Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 687)

Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Hollman, M., Hultman, M., Kucaba, T., Leh., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liltopsida; Poales; Poaceae; Oryza.
1 (bases 1 to 493)
Sasaki,T., Miyao,A. and Yamamoto,K.
                                                                                                             365 gaaacagttgctgnaagctaccttgagtttgcccaagaaacccttnatnag 415
                                                                                                                                                 64 GAAACGITICCICCAAAGIACCIICAIIAIGACGAAGAAACCICICAICAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 493;
                         Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 others
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Pred. No. 6.10e-06;
0; Mismatches 19; Indels
                                                                  0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Institute of Agrobiological Resources 2-1-2 Kanondai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Nipponbare"
/dev_stage="Green shoot (8 days old)"
147 c 150 g 93 t 5 ot)
                      Score 22; DB 57; 1
Pred. No. 6.10e-06;
                                                                                                                                                                                                                 RICS15559A 493 bp mRNA
Rice CDNA, partial sequence (S15559_1A).
D48963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki,T., Miyao,A. and Yamamoto, K. stee CDNA from shoot Unpublished (1995)
PROJECT = RGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-Feb-1995) to DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                    y Match 5.0%;
Local Similarity 68.6%;
hes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.0%;
Best Local Similarity 66.1%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Japan 305
Phone: 0298-38-7441
Fax : 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsukuba Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..493
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                         Query Match
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AUTHORS
                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
Broaryotaes: Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;
Brassicaceae; Arabidopsis.
1. (bases 1 to 472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                      Email: est@watson.wustl.edu
High quality sequence stops: 321
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-AUG-1995
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MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                        4444 Förest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 111; Length 453;
Pred. No. 6.10e-06;
0; Mismatches 9; Indels
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142477
19933235
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                                        Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 t
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MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"/clone="264865"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="113K15T7"
/strain="var columbia"
97 c 100 g
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Best Local Similarity 77.5%;
Matches 31; Conservative
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66
Unpublished (1995)
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Gaps

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/note="Organ: eye; Vector: lambda gt10; Site_1: EcoRI; Site_2: EcoRI; The library used for sequencing was a sublibrary derived from a human retina cDNA library. Inserts from retina cDNA library DNA were isolated, randomly primed, PCR amplified, size-selected, and cloned into lambda gt10. Individual plaques were arrayed and used as templates for PCR amplification, and these PCR
                                                                                                                                                                                                                                                                                                                                                                                                   Length 796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELKO94GZR 317 bp mRNA EST 1
C.elegans cDNA clone yk94g12 : 3' end, single read.
D66283
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                                                                                                                                                                                                                                                                                                                                   56 others
                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 117; Length 79
Pred. No. 6.10e-06;
0; Mismatches 12; Indels
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/clone_lib="ruji kohara unpublished cDNA"
82 c 64 g 85 t 7 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 totoctgottottgatototocactotacatocaacoggnaagotoot 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 GCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCACAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toward an expression map of the C.elegans genome Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                         /dev_stage="adult"
/lab_host="E. coli strain K802"
<1..>796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="CB1489 him-8(e1489)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-Aug-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Hermaphrodite, male"
                                                                                                                                                                                                                                      /tissue_type="retina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute of Genetics
Vata 1111, Mishima Shizuoka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email:ykohara@ddbj.nig.ac.jp.
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Best Local Similarity 70.8%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 y Match 5.0%;
Local Similarity 73.9%;
nes 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 0559-81-6855
                                                                                                                                                                                                                                                                                                                                 181 c
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Gene Library Lab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishigaki,A.
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Matches
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Aparmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTyT3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
/clone="487938"
/clone_lib-"Soares pregnant uterus NbHPU"
                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMIS clone is available royalty-free through LLNL; contact the
TMIS Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd, from Amersham
High quality sequence stop: 477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W29026 796 bp mRNA EST 08-MAY-1996
55clO Human retina cDNA randomly primed sublibrary Homo sapiens
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
JSS North Wolfe Street, Baltimore, MD 21205
Tel: 410 955 4687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 22; DB 137; Length 687;
Pred. No. 6.10e-06;
0; Mismatches 11; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 atacatatcagtctgcttttgtcatcttctgcagtgagcttccaacactcc 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 ATACATATCTGTG-GCTTGGGTCTTCTCCTGCATCCAGCTTGCACCACTCC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: CTTTTGAGCAAGTTCAGCCTGGTTAAGT
BACKWARD: GAGGTGGCTTATGAGTATTTCTTCCAGGGTAA
Seq primer: GGGTAAAAAGCAAAAGAATT.
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Macke, J., Smallwood, P. and Nathans, J.
Adult Human Retina cDNA
Unpublished (1996)
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 5.0%;
Best Local Similarity 76.5%;
Matches 39; Conservative
                     Contact: Wilson RK
                                                                                                                                                                                                                                                                                                      ...687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR PRimers
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products were used for sequencing."
/clone_lib="Human retina cDNA randomly primed sublibrary"
/sex="mixed (males and females)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BILIGE74
BIRCHARDER SEQUENCE tag).
BIRCHARDER SEQUENCE tag).
Caenorhabditis elegans (strain CB1489 him-8(el489), ) (library:
Vuji kohara unpublished cDNA) Hermaphrodite, male varied whole animal CDNA to mRNA.
Caenorhabditis elegans
BUKARYOTAE, mitochondrial eukaryotes; Metazoa; Nematoda;
Secennentea; Rhabditia; Rhabditida; Rhabditidae; Caenorhabditis.

Rhabditidae; Caenorhabditis.

1 (bases 1 to 317)
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/organism-"Homo sapiens"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI; Reference: Hum Mol Gen 2, 1795 (1993)
Takeda et al. Cloned unidirectionally. Primer: Oligo dT.
-5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor
/clone="3228959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-00T-1996 mRNA EST 17-00T-1996 5c08h02 membrane-free polysomes from endosperm Zea mays cDNA clone 123370 95 end. 9511392
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Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
ph: 602-6218-746
fax: 602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 360)
Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,
Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1169 Std Error: 0.00 Seq primer: mob.REGA+FT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Biological Sciences, School of Science California State University, Hayward
                                                                                                                                                                                                                                                                                                                                                     /clone_lb="Pancreatic Islet"
/tissue_type="pancreatic islet"
/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 1.34e-04;
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E-mail: cbaysdor@s1.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E-mail: helnjars@ccit.arizona.edu
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                                                                                                                                                        Location/Qualifiers
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                                            Email: est@watson.wustl.edu
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Best Local Similarity 76.9%;
Matches 30; Conservative
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ph: 510-881-3459
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                   human clone=73829 library=Stratagene fetal spleen (#937205)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=M13RP1 Rsitel=EcoRI Rsite2=RhoI Pooled fetal spleens. Cloned
unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb;
uni-ZAP XR Vector; 5' adaptor sequence: 5'-GAATTGGCACGAGG-3'; 3'
adaptor sequence: 5'-CTCGAGTTTTTTTTTTTTTTTTTTT"3'.
                                                                                                                                                                                                                                                                                                    Eucaryotae: Metazoa: Chordata: Vertebrata; Gnathostomata: Mammalia; Eutheria: Primates: Catarrhini; Hominidae; Homo.
1 (Bases I to 325)
1 (Bases I to 325)
Hiller.L. Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 328) Hiller, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Riffin, L., Rohlfing, T., Tan, F., Trevaskis, E., Wasterston, K., Williamson, A., Wohldmann, P. and Wilson, R. Unpublished (1995)
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2C82h06.rl Pancreatic Islet Homo sapiens CDNA clone 328859 5/
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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              yb42d03.rl Homo sapiens CDNA clone 73829 5' similar to gb:J03910_rnal Human (HUMAN).
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Pred. No. 1.34e-04;
0; Mismatches 8;
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WashU-Merck EST Project
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Matches 29; Conservative
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Marta,M., Sibley,L.D., Wan,K.L. and Waterston,R.A.
Washh-Merck Toxoplasma EST Project
Unpublished (1996)
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Toxoplasma gondii
Eukaryotae; mitochondrial eukaryotes; eukaryote crown group;
Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystida;
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Interdisciplinary Center for Biotechnology Research
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Pred. No. 1.34e-04;
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                                                                                                                                             E-mail: robferlnervm.nerdc.ufl.edu
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/strain="W64A2"
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                                                                               Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
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                     DNA Sequencing Core
University of Florida
P.O. Box 100695
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Best Local Similarity 83.3%;
Matches 25; Conservative
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Tel: 314 286 1800
Fax: 314 286 1810
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DEFINITION yC50d04.rl Homo sapiens cDNA clone 84103 5' similar to
95:J03910_rnal Human (HUMAN);.
ACCESSION T71088
NID 9685609
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WashU-Merck EST Project
Washington University School of Medicine
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/organism="Toxoplasma gondii"
/clone="tgzy27b03.r1"
/strain="RH"
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Matches 33; Conservative
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Best Local Similarity 78.4%;
Matches 29; Conservative
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Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
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                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
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                                 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                                                                                                                                                                                      Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopteraydi: Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 383)
14 (last, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Materston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stops: 268 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human clone=188313 library=Soares breast 3NbHBst vector=pT7T3D
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1 (bases 1 to 395)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T71079 395 bp mRNA EST 01-MA
Yc50c04.r1 Homo sapiens cDNA clone 84102 5' similar to
gb:J03910_rnal Human (HUMAN);.
g685600
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...34e-6; Indels
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                                                                                                                                                                                     and M.Fatima Bonaldo.
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Local Similarity 81.8%;
les 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
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KEYWORDS
SOURCE
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High qulity sequence stops: 304
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                     Contact: Wilson RK
WashU-Merck EST Project
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 others
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Pred. No. 1.34e-04;
0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/clone="84102"
105 c 91 g 110
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                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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WashU-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 78.4%;
Matches 29; Conservative
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Human chromosome 5 LA Human chromosome 5 LA Human chromosome 5 LA 26232 Lambda-PRL2 Ara human STS SHGC-7175 c zr55911.s1 Soares NhH

ATA67387 G14220 HS1147657

446 440 440 440 63 63 83

Human chromosome 5 LA

5740 Arabidopsis thal

AA219045

Description

DB

Match Length

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64:qnest21 66:qnest12 66:qnest18 67:qnest19 68:qnest25
69:qnest21 70:qnest2 71:qnest23 72:qnest12 87:qnest25
74:qnest7 75:qnest1 76:qnest2 77:qnest3 78:qnest2
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84:qnest7 80:qnest1 86:qnest1 87:qnest18 83:qnest19
84:qnest15 90:qnest1 86:qnest17 92:qnest18 83:qnest19
94:qnest25 100:qnest21 96:qnest27 77:qnest21 98:qnest219
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23:EST221 24:EST22 25:EST223 26:EST224 27:EST225

28:EST222 29:EST223 36:EST223 36:EST239 32:EST230

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39:STS4 40:STS5 41:STS6 42:STS7 43:STS8 44:STS9 45:STS10
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                                                                                                                                                                                                                                                                                                                                               Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.
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TACTTGTTCAACGACACGAC.
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(1-438) from US08915004.seq
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human STS SHGC-32985. LD04428.5prime LD Dro

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mu36c04.rl mm52b05.rl

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AA209457 AA068479 AA202414 AA246779

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zp86cll.rl stratagene zn55(02.rl Stratagene m95f06.rl Stratagene yv55cl2.rl Soares fet nc38f10.rl NCI CGAP P nc38f10.rl NCI CGAP P nc38f10.rl NCI CGAP P

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AA228313 AA202904

zn69a03.s1 Stratagene

zr55g11.sl Soares zt30e09.sl Soares zt30e09.sl Soares

HS1153832

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Newman T., deBruijn F.J., Green P., Keegstra K., Kende H., McIntosh L., Ohlrogge J., Raikhel N., Somerville S., Thomashow M., Retzel E., Somerville C.; Retzel E., Somerville C.; Referes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae, mitochondrial eukaryotes, Viridiplantae,
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                          9933235
02-FEB-1995 (Rel. 42, Created)
12-MAR-1997 (Rel. 51, Last updated, Version 15)
5740 Arabidopsis thaliana cDNA clone 113K15T7.
                                                                                  standard; RNA; EST; 472 BP.
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Plant Physiol. 106:1241-1255(1994).
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RESULT 11
AC 744774
NI 9933235
DT 02-FEB-10
DE 5740 Arg
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OC Charoph,
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

& Query

Result

3.14e-02 3.14e-02 3.14e-02

Stratagene Beddington

zq43e07.s1 mo80h01.r1

AA191607 AA208979

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -41ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 431).
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
  AGIS; | 142477; AGIS July 1995.
Contaçt: Thomas Newman MSU-DOE Plant Research Laboratory Michigan
                                                  State University MSU-DOE-PRL, Michigan State University, Plant
Biology Bldg.,E. Lansing,Mi Tel: 517-353-0854 Fax: 517-353-9168
Email: 22313tcn@lbm.cl.msu.edu. NCBI gi: 933235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                   /strain="var columbia"
/note="thale cress"
Sequence 472 BP; 126 A; 97 C; 100 G; 137 T; 12 other;
                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/clone="113K15T7"
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Pred. No. 1.04e-04;
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                                                                                                                                 Location/Qualifiers
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Best Local Similarity 71.7%;
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 68.6%;
Matches | 35; Conservative
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Fax: 314 286 1810
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Homo sapiens (tissue library: LANL flow sorted chromosome 5 library in M13mp18) DNA. Homo sapiens
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/tissue_lib="LANL flow sorted chromosome 5 library in
M13mp18"
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/tissue_lib="LANL flow sorted chromosome 5 library in
M13mpl8"
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 204)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grady D.L., Robinson D.L., Gersh M., Nickerson E., McPherson J., Wasmuth J.J., Overhauser J., Deaven L.L., Moyzis R.K.; The generation and regional localization of 303 new chromosome sequence-tagged sites; Genomics 32:91-96(1996).
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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           0; Mismatches 13; Indels
                                                          296 gcaaggaaatgcagtattttatgcagcagtggactgntaccaacaa 341
                                                                                                  260 GCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCACAA 305
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                                                                                                                                                                                                                                    g1160700
24-JAN-1996 (Rel. 46, Created)
18-MAR-1997 (Rel. 51, Last updated, Version 3)
Human chromosome 5 LANL STS 200.
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/evidence=EXPERIMENTAL
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/evidence=EXPERIMENTAL
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Local Similarity 72.7%;
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/organism-"Arabidopsis thaliana"
/strain-"var columbia"
/strain-"vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRLZ is a CDNA library derived from equal quantitie
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Wasmuth,J.J., Overhauser,J., Deaven,L.L. and Moyzis,R.K.
The generation and regional localization of 303 new chromosome sequence-tagged sites
Genomics 32 (1), 91-96 (1996)
96230329
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Ml3mp18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E. Lansing,Mi Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@ibm.cl.msu.edu Seg primer: T7.
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Charophyta/Embryophyta group: Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
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12-MAR-1997 (Rel. 51, Last updated, Version 5)
26232 Lambda-PRL2 Arabidopsis thaliana cDNA clone 88F5T7.
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                                                                                                                  /organism="Homo sapiens"
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/evidence=experimental
/note="for primer B"
47 c 38 g
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                                                                                     Location/Qualifiers
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MEDLINE
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 204)
Grady, D.L., Robinson, D.L., Gersh, M., Nickerson, E., McPherson, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/tissue_lib="LANL flow sorted chromosome 5 library in
M13mp18"
                                                                                                                                                                                                                                                                                                                                                     10-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-1997
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 204)
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                                                                                                                                                                                                                   0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Indels
                                                                                                                                                                                                                                                    71 tgtcacacaacaccaaatcatagctttccacatcaatctgaagg 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 tgtcacacaacaccaaatcatagctttccacatcaatctgaagg 114
                                                                                                                                                                                                                                                                      84
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                                                                                                                                                                                  Score 20; DB 46; Pred. No. 1.93e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.93e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 47;
               /standard_name="LANL STS 200"
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                                                           /note=for primer A"
172..197
/evidence=experimental
/note="for primer B"
a 47 c 78 g g 6
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Human chromosome 5 LANL STS 200.
L28249
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Human chromosome 5 LANL STS 200.
L28249
                               complement(2..26)
/evidence=experimental
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Unpublished (1995)
                                                                                                                                                                                  Query Match 4.6%;
Best Local Similarity 72.7%;
Matches 32; Conservative
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Local Similarity 72.7%;
nes 32; Conservative
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Homo sapiens
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TINITION
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ORIGIN
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AUTHORS
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FEATURES
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SOURCE
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Matches

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ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

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Gaps

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/note="Organ: mixed (see below); Vector: pT7T3D-Pac /hote="Organ: mixed (see below); Vector: pT7T3D-Pac /bParmacial) with a modified polylinker; Site_1: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares NhHMPu S1" /tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Barsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; "The Washu-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest park way, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Email: Email: est@watson.wustl.edu This clone is available royalty-free through LLL.; contact the IMAGE Consortium (infedimage.lln.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -41m13 fwd. ET from Amersham High quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-1997 (Rel. 51, Created)
27-FEB-1997 (Rel. 51, Last updated, Version 1)
27-FEB-1997 (Rel. 51, Last updated, Version 1)
27-FEB-1997 (Rel. 51, Last updated, Version 1)
27-FEB-1997 (Rel. 51, Last updated)
27-FEB-1997 (Rel. 51, Last updated)
27-FEB-1997 (Rel. 51, Created)
27-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 417;
                                                                                                                                                                                                                                     Length 400;
                                                                                                                                                    16 others
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/lab_host_with101
mRNA
complement(<1.>>417)
Sequence 417 BP; 102 A; 90 C; 115 G; 109 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                     177 acaccactgtactccagcctggaagacagagtgagacct 216
                                                                                                                                                                                                                                                                                                                                                                                                            153 ACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCT 192
                                                                                                                                                                                                                                     Score 20; DB 40;
Pred. No. 1.93e-03;
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Pred. No. 1.93e-03;
0; Mismatches 2;
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/map="3"
255..275
/map="3"
complement(328..348)
/map="3"
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HS1147657 standard; RNA; EST; 417 BP.
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                                                                                                                                                 90 9
                                                                                                                                                                                                                                     Query Match 4.6%;
Best Local Similarity 75.0%;
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Best Local Similarity 91.7%;
Matches 22; Conservative
                                                                                                                                                 95 C
                                                                                                                                                                                                                                                                                            30; Conservative
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                                 primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA228090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Bukaryotee mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
   directionally cloned with Sal-Notarms using oligo dT prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 3 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institue for Medical Research, Camden, NJ 08103.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial incubation: 94 degrees C for 90 seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
                                                                                                                                                                                                                                     Length 377;
                                                                                                                                                                                                                                                                                         0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30
Perkin Elmer 9600
                                                                              /Clone="88F5T7"
/Clone_11b="Lambda-PRL2"
-(1..>377
Sequence 377 BP: 100 A: 93 C: 64 G: 105 T: 15 other;
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                                                                                                                                                                                                                                                                                                                                                     tgcacaantgcaaccacaaccgcaatcgcagccacaaccgc 217
                                                                                                                                                                                                                                                                                                                                                                                       269 TGCAGTACGTCAAGCAGGAGTGCAATCGCACACAAACCGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STS sequence; primer; sequence tagged site.
                                                                                                                                                                                                                                  Score 20; DB 79; 1 Pred. No. 1.93e-03;
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Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G14220 400 bp DNA
human STS SHGC-7175 clone pG-3149.
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                                                                                                                                                                                                                                                           Pred. No. 1.
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Primer B: GTCAACTCAGGCATTCCTACT
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50 mM
20 mM
8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catarrhini; Hominidae; Homo.
1 (bases 1 to 400)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR Cycles:
Thermal Cycler:
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                                                                                                                                                                                                                                                              Local Similarity 73.2%;
nes 30; Conservative
                                                                                                                                                                                                                                     4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Annealing:
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pH:
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                                                            CDNA."
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PCR Profile
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88 aaaacaacactgtagagaaaagtg 111
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                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
WashU-Merck EST Project
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Best Local Similarity 91.7%;
                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
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                                  PRECURSOR ; . AA235526 g1859981
                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                   human.
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HS1153832
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHz, pregnant uterus
NbH9U, and fetal heart NbHH19W) were mixed and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-348479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 332.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares NhHMPu S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 417)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hutanen, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                   AA228090 417 bp mRNA EST 24-FEB-1997 zr55g11.s1 Soares NhHMPU S1 Homo sapiens cDNA clone 667364 3' similar to TR:G307146 G307146 PROTEIN-LXSINE OXIDASE HOMOLOG
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Pred. No. 1.93e-03;
0; Mismatches 2; Indels
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                      150 AAAACAACACTGTACAGCAAAGTG 173
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Best Local Similarity 91.7%;
Matches 22; Conservative
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AUTHORS
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/Organism="Homo sapiens"
/Organism="Homo sapiens"
/Organism="Homo vary; Vector: pT713D (Pharmacia) with a modified polylinker; Site.]: Not I: Site.2: Eco RI: 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' double-Etranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT713 vector M.Fatima Bonaldo."
//Clone="723880"
zt30e09.sl Soares ovary tumor NDHOT Homo sapiens cDNA clone 723880
3' similar to TR:G307146 G307146 PROTEIN-LYSINE OXIDASE HOMOLOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: 41m13 fwd. ET from Amersham
High quality sequence stop: 174.
                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 421)
Hilller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trewskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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06-MAR-1997 (Rel. 51, Last updated, Version 1)
2t30e09.sl Soares ovary tumor NbHOT Homo sapiens cDNA clone 723880
3' similar to TR:G307146 G307146 PROTEIN-LYSINE OXIDASE HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/lab_host="DH10B (ampicillin resistant)"
complement(<1..>421)
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Pred. No. 1.93e-03;
0; Mismatches 2;
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The WashU-Merck EST Project
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Unpublished

source

1-421

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/hote-vector: paluscript SK-; Site_1: EcoRI; Site_2: Xhois-cloned unidirectionally. Primer: Oligo dr. HeLa S3 epithelioid carcinoma cells grown to semi-confluency without induction. Average insert size: 1.5 kb; Uni-ZAP XR Vector. -5' adaptor sequence: 5' GAATYCGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3' -/ Clone_1ib="Stratagene HeLa cell s3 937216"

        LOCUS
        AA191137
        424 bp
        mRNA
        EST
        15-JAN-1997

        DEFINITION
        zp86c11.rl
        Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 67092 S.
        627092 S.

        AACESSION
        AA191137

        NID
        91779831

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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@linage.llnl.gov) for further information. Seq primer: -40K13 fwd. from Amersham High quality sequence stop: 353.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 414)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/lab_host="SOLR (kanamycin resistant)"
complement(<1..>423)
121 t 3 othe
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Pred. No. 1.93e-03;
0; Mismatches 6.
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Local Similarity 81.3%;
les 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zn69a03.s1 Stratagene HeLa cell s3 937216 Homo sapiens CDNA Clone 563404 3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                       Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Barsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
"The washu-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 53100 Tel: 314 286 1800 East; Blu Demail Est Demails est@watcon.wustl.edu This clone is available royalty-free through LINI contact the IMAGE Consortium (info@image.llnl.gov) for turther information. Possible reversed clone: similarity on wrong strand Seg primer: -41ml3 fwd. ET from Amersham High quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                       Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.6%, Score 20; DB 83; Length 421;
Best Local Similarity 91.7%; Pred. No. 1.93e-03;
Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="ovarian tumor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares ovary tumor NbHOT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 aaaacaacactgtagagaaaagtg 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 bp
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DEFINITION

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ACCESSION

KEYWORDS

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Gaps

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AA211552 503 bp mRNA EST 31-JAN-1997
zn55f02.rl Stratagene muscle 937209 Homo sapiens cDNA clone 562107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
WashU-Merck EST Project
WashU-Merck EST Project
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28m13 revl ET from Amersham
High quality sequence stop: 440.
                                                                                                                                                                                                                                                                                                                                                                                Homo saplens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
1 (bases 1 to 503)
Hilliar.L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultnan,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Unpublished (1995)
                                                                                                                             Gaps
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                                                                                        Length 424;
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                                                                                     Score 20; DB 15; Length 424 Pred. No. 1.93e-03; 0; Mismatches 4; Indels
/lab_host="SOLR (kanamycin resistant)"
<1..>424
1 119 c 111 g 90 t 5 oth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="552107"
/clone_lib="Stratagene muscle 937209"
/dev_stage="adult"
/lab_lost="SOLR (kanamycin resistant)"
                                                                                                                                                    111 g
                                                                                   Query Match 4.6%;
Best Local Similarity 85.7%;
Matches 24; Conservative
                                99 a
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91810206
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       mRNA
BASE COUNT
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                               EYWORDS
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Gaps ö Query Match
4.6%; Score 20; DB 22; Length 503;
Best Local Similarity 85.7%; Pred. No. 1.93e-03;
Matches 24; Conservative 0; Mismatches 4; Indels

5 others

104 t

135 g

<1..>503

BASE COUNT ORIGIN

mRNA

257 caaggagctgcagtcggtggagcaggag 284 g

261 CAAGGAGCTGCAGTACGTCAAGCAGGAG 288 ò

Search completed: Tue Dec 2 17:31:35 1997 Job time: 172 secs.

